

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 6, 2005, 05:47:32 ; Search time 181.5 Seconds  
(without alignments)  
6622.872 Million cell updates/sec

Title: US-10-032-254A-1  
Perfect score: 2872  
Sequence: 1 gttgcggagtcctccactc.....caaaaaaaaaaaaaaa 1554

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2105692 seqs, 386760381 residues  
Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ n2p.model -DEV=xlp  
-Q=/cgn2\_1/USPTO\_spool\_p/US10032254/runat\_02062005\_131018\_3585/app\_query.fasta\_1.1735  
-DB=A Geneseq\_16Dec04 -Qfmt=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10032254 @CGN\_1\_1\_154 @runat\_02062005\_131018\_3585 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : A Geneseq\_16Dec04: \*  
1: geneseqp1980s: \*  
2: geneseqp1990s: \*  
3: geneseqp2000s: \*  
4: geneseqp2001s: \*  
5: geneseqp2002s: \*  
6: geneseqp2003as: \*  
7: geneseqp2003bs: \*  
8: geneseqp2004s: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1808	63.0	358	2 AAW50159	AAW50159 Calmoduli
2	1690	58.8	343	4 AAU03511	Aau03511 Human pro
3	1673.5	58.3	372	5 ABP69106	Abp69106 Human pol
4	1673.5	58.3	372	8 ADR39752	Adr39752 Human kin
5	1625	56.6	343	2 AAW88436	Aaw88436 Disease a
6	1625	56.6	343	8 ADL06509	Adl06509 Human tum
7	1625	56.6	343	8 ADM72655	Adm72655 Human TAS
8	1625	56.6	343	8 ADM72237	Adm72237 Human TAS
9	1259	43.8	270	6 ABR41269	Abr41269 Human DIT
10	1204	41.9	250	6 ABR41299	Abr41299 Human DIT

11	1184.5	41.2	332	7	ADC15044	Adc15044 Calcium/c
12	1184.5	41.2	370	6	AAE34492	Aae34492 Human cam
13	1184.5	41.2	370	8	ADH23304	Adh23304 Human cal
14	1184.5	41.2	370	8	ADL97820	Adl97820 Human CAM
15	1184.5	41.2	370	8	ADP23704	Adp23704 PRO polyp
16	1182.5	41.2	317	5	ABG69794	Abg69794 Human CAM
17	1173.5	40.9	355	4	AAE11777	Aae11777 Human kin
18	1173.5	40.9	355	4	AAM41268	Aam41268 Human pol
19	1173.5	40.9	355	5	ABB08178	Abb08178 Human CaM
20	1173.5	40.9	357	4	AAE11768	Aae11768 Human kin
21	1173.5	40.9	357	8	ADJ75440	Adj75440 Marker ge
22	1173.5	40.9	357	8	ADQ15044	Adq15044 Human can
23	1173.5	40.9	385	4	AAM39482	Aam39482 Human pol
24	1173.5	40.9	385	4	AAB84359	Aab84359 Amino aci
25	1169.5	40.7	355	4	AAB50055	Aab50055 Murine De
26	1168.5	40.7	357	4	AAU03508	Aau03508 Human pro
27	1157	40.3	356	4	AAH84360	Aah84360 Amino aci
28	1112	38.7	355	8	ADI40885	Adi40885 Human kin
29	1085.5	37.8	389	3	AAH68793	Aay68793 Amino aci
30	1070	37.3	503	4	ABG05970	Abg05970 Novel hum
31	1065	37.1	460	5	ABG69792	Abg69792 Human CAD
32	1065	37.1	476	5	AAE22764	Aae22764 Human cal
33	1065	37.1	476	5	ABG69793	Abg69793 Human CAD
34	1065	37.1	476	7	ADE56391	Ade56391 Human Pro
35	1065	37.1	476	7	ADE56387	Ade56387 Human Pro
36	1065	37.1	476	7	ADD45328	Add45328 Human Pro
37	1065	37.1	497	4	AAM41547	Aam41547 Human pol
38	1051.5	36.6	567	4	AAH39761	Aam39761 Human pol
39	1028.5	35.8	309	7	ADE56389	Ade56389 Rat Prote
40	1028.5	35.8	309	7	ADD45326	Add45326 Rat Prote
41	1028.5	35.8	309	7	ADE56385	Ade56385 Rat Prote
42	1028.5	35.8	309	7	ADD46031	Add46031 Rat Prote
43	1017.5	35.4	326	6	AAE32426	Aae32426 Human kin
44	1017.5	35.4	326	8	ADE28335	Ade28335 Human KPP
45	1017.5	35.4	326	8	ADH23302	Adh23302 Novel hum

ALIGNMENTS

RESULT 1		AAW50159	
ID	AAW50159	standard; protein; 358 AA.	
XX	AAW50159;		
AC	AAW50159;		
XX			
DT	09-JUL-1998	(first entry)	
XX			
DE	Calmodulin-dependent protein kinase clone 29.		
XX			
KW	Rat; calmodulin-dependent protein kinase; clone 29.		
XX			
OS	Rattus rattus.		
XX			
FH	Key	Location/Qualifiers	
FT	Misc-difference 344		
FT	/note= "encoded by TG"		
XX			
PN	WO9805352-A1.		
XX			
PD	12-FEB-1998.		
XX			
PF	01-AUG-1997;	97WO-US013657.	
XX			
PR	02-AUG-1996;	96US-0023220P.	
XX			
PA	(SCRI )	SCRIPPS RES INST.	
XX			
PI	Sutcliffe JG,	Gautvik KM, De Lecea L, Bloom FE, Danielson PE;	
PI	Gautvik VT,	Kilduff TS, Foye PE;	
XX			
DR	WPI; 1998-145352/13.		
DR	N-PSDB; AAV18867.		
XX			

PT Nucleic acid encoding hypocretin of rat and mouse - useful for diagnosis  
PT and treatment of neurological disease, homeostatic dysfunction etc., also  
PT sequence for calmodulin kinase-like protein.

XX Disclosure; Fig 6; 11lpp; English.  
XX The present sequence is rat calmodulin-dependent protein kinase clone 29.  
XX Sequence 358 AA;  
SQ

Alignment Scores:  
Pred. No.: 2.26e-141 Length: 358  
Score: 1808.00 Matches: 353  
Percent Similarity: 98.60% Conservative: 0  
Best Local Similarity: 98.60% Mismatches: 5  
Query Match: 62.95% Indels: 1  
DB: 2 Gaps: 0

US-10-032-254A-1 (1-1554) x AAW50159 (1-358)  
QY 105 ATGCTGTGCTCAAGAAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAAG 164  
Db 1 MetLeuLeuLeuLysLysGlnThrGluAspIleSerSerValTyrGluIleArgGluLys 20  
QY 165 CTGGGCTCGGTGCCTTCTCTGAGGTGATGCTGGCCCCAGGAAGGGGCTCTGCTCATCTT 224  
Db 21 LeuGlySerGlyAlaPheSerGluValMetLeuAlaGlnGluArgGlySerAlaHisLeu 40  
QY 225 GTGGCCCTCAAGTGCATTCCCAAGAACCACTTCGGGGCAAGGAGCCCTGGTGGAGAAAT 284  
Db 41 ValAlaLeuLysCysIleProLysLysAlaLeuArgGlyLysGluAlaLeuValGluAsn 60  
QY 285 GAGATCGGGTACTTCGCAGAAATCAGCCATCCCAACATTGTGGTCTCTGGAGGACGTCCAT 344  
Db 61 GluIleAlaValLeuArgArgIleSerHisProAsnIleValAlaLeuGluAspValHis 80  
QY 345 GAGAGTCCTTCTCATCTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAACGTGTTGAC 404  
Db 81 GluSerProSerHisLeuTyrLeuAlaMetGluLeuValThrGlyGlyGluLeuPheAsp 100  
QY 405 CGCATCATGGAGCGGGGCTCCTACACAGAGAAGGACGCCAGCCTTGTAGGGCAGGTC 464  
Db 101 ArgIleMetGluArgGlySerTyrThrGluLysAspAlaSerHisLeuValGlyGlnVal 120  
QY 465 CTTGGCGCTGTCTCCTACCTTCATAGCTGGGCATCGTGCACCGGGACCTCAAGCCTGAA 524  
Db 121 LeuGlyAlaValSerTyrLeuHisSerLeuGlyIleValHisArgAspLeuLysProGlu 140  
QY 525 AACCTCCTCATGCCACACCTTTTGAGGACTCCAAGATCATGGRCTCTGACTTTGGCCTG 584  
Db 141 AsnLeuLeuTyrAlaThrProPheGluAspSerLysIleMetValSerAspPheGlyLeu 160  
QY 585 TCCAAATACAAGCTGGCAACATGCTAGGCACAGCCTGTGGGACCCCAAGGATATGTGGCC 644  
Db 161 SerLysIleGlnAlaGlyAsnMetLeuGlyThrAlaCysGlyThrProGlyTyrValAla 180  
QY 645 CCAGAGCTCTGGAGCAGAAACCCCTACGGGAAGGCCGTAGATGTGTGGGCCCTGGGTGC 704  
Db 181 ProGluLeuLeuGluGlnLysProTyrGlyLysAlaValAspValTrpAlaLeuGlyVal 200  
QY 705 ATCTCCTACATCCTGTGTGGGTACCCCCCTTCTATGATGAGAGCGATCCTGAATC 764  
Db 201 IleSerTyrIleLeuLeuCysGlyTyrProProPheTyrAspGluSerAspProGluLeu 220  
QY 765 TTCAGCCAGATTCTGAGGGCCAGCTATGAGTTTGACTCCCCCTTTGGGATGACATCTCA 824  
Db 221 PheSerGlnIleLeuArgAlaSerTyrGluPheAspSerProPheTrpAspIleSer 240  
QY 825 GAATCAGCCAAAGACTTCATTTCGCCACCTTCTTGGAACGTGATCCCCAGAGAGGTTTACC 884  
Db 241 GluSerAlaLysAspPheIleArgHisLeuLeuGluArgAspProGlnLysArgPheThr 260  
QY 885 TGCCAGCAGGCCCTACAGCATCTTTGGATCTCTGGGGATGCAGCCTTCGATAGGGACATC 944

Db 261 CysGlnGlnAlaLeuGlnHisLeuTrpIleSerGlyAspAlaAlaLeuAspArgAspIle 280  
QY 945 CTGGGTTCTGTGAGTGAGCAGATCCAGAAGAAATTTTGCAGGACCCACTGGAAGCGTGCA 1004  
Db 281 LeuGlySerValSerGluGlnIleGlnLysAsnPheAlaArgThrHisTrpLysArgAla 300  
QY 1005 TTCAATGCCACATCATCTCTACGTACGTACATCCGTACGTCAGCCACCCAGGCTTGGGACTAGCCAGTCC 1064  
Db 301 PheAsnAlaThrSerPheLeuArgHisIleArgLysLeuGlyGlnSerProGluGlyGlu 320  
QY 1065 GAGGCCTCCAGGCAGTGTATGACCCGTATGACCCGTATGACCCAGGCTTGGGACTAGCCAGTCC 1124  
Db 321 GluAlaSerArgGlnGlyMetThrArgHisSerHisProGlyLeuGlyThrSerGlnSer 340  
QY 1125 CCCAAGTGGTG-AAAACCAGGTAGATGCCAAGGAAGGCCAAGTGGACTGACTCC 1177  
Db 341 ProLysTrpValThrThrArgTrpMetProArgLysAlaLysTrpThrAspSer 358

RESULT 2  
AAU03511  
ID AAU03511 standard; protein; 343 AA.  
XX  
AC AAU03511;  
XX  
DT 12-SEP-2001 (first entry)  
XX  
DE Human protein kinase #11.  
XX  
KW Human; protein kinase; PTK; STK; cancer; cardiovascular disease;  
KW metabolic disorder; immune related disease; neurological disorder;  
KW neurodegenerative disorder; inflammatory disorder; infectious disease;  
KW reproductive disorder.  
XX  
OS Homo sapiens.  
XX  
PN WO200138503-A2.  
XX  
PD 31-MAY-2001.  
XX  
PF 22-NOV-2000; 2000WO-US032085.  
XX  
PR 24-NOV-1999; 99US-0167482P.  
XX  
PA (SUGE-) SUGEN INC.  
XX  
PI Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;  
PI Flanagan P, Clary D;  
XX  
DR WPI; 2001-343950/36.  
XX  
DR N-PSDB; AAS06711.  
XX  
PT Nucleic acids encoding human kinase polypeptides, useful for preventing  
PT diagnosing and/or treating e.g. cancer, immune, cardiovascular and  
PT neuronal-associated diseases, and microbial infections.  
XX  
PS Claim 7; Fig 2; 433pp; English.  
XX  
CC AAU03501-AAU03557 represent novel human protein kinases #1-57. The novel  
CC protein kinases have been identified as members of the tyrosine or  
CC serine/threonine kinase (PTK and STK) families. The polynucleotides  
CC encoding protein kinases and the polypeptides may be used in the  
CC prevention, diagnosis and treatment of diseases associated with  
CC inappropriate kinase expression. For example, they may be used to treat  
CC cancers (especially cancers of haematopoietic origin), cardiovascular  
CC disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),  
CC immune related diseases (e.g. rheumatoid arthritis), neurological  
CC disorders (e.g. schizophrenia), neurodegenerative disorders (e.g.  
CC parkinson's disease), inflammatory disorders (e.g. asthma), infectious  
CC disease (e.g. HIV) and reproductive disorders (e.g. infertility).  
CC Additionally, polynucleotides encoding protein kinases may be used for  
CC gene therapy and as DNA probes in diagnostic assays. The protein kinase  
CC polypeptides may be used as antigens in the production of antibodies

CC against the protein kinases and in assays to identify modulators of  
CC protein kinase expression and activity

XX  
SQ Sequence 343 AA;

Alignment Scores:

Pred. No.: 1.46e-131 Length: 343  
Score: 1690.00 Matches: 325  
Percent Similarity: 96.21% Conservative: 5  
Best Local Similarity: 94.75% Mismatches: 13  
Query Match: 58.84% Indels: 0  
DB: 4 Gaps: 0

US-10-032-254A-1 (1-1554) x AAU03511 (1-343)

QY 105 ATGCTGTGCTCAAGAAACAGACGGAGGACATCAGCAGTGTCTATGATCCGGGAGAAG 164  
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Db 1 MetLeuLeuLeuLysHisThrGluAspIleSerSerValTyrGluIleArgGluArg 20  
  
QY 165 CTGGGCTCGGTGCCTTCTCTGAGGTGATGCTGGCCAGGAAAGGGCTCTGCTCATCTT 224  
|||||  
Db 21 LeuGlySerGlyAlaPheSerGluValValLeuAlaGlnGluArgGlySerAlaHisLeu 40  
  
QY 225 GTGGCCCTCAAGTGCATTCCCAAGAAACACTTCGGGGCAAGGAGCCCTGGTGAGAAAT 284  
|||||  
Db 41 ValAlaLeuLysCysIleProLysLysAlaLeuArgGlyLysGluAlaLeuValGluAsn 60  
  
QY 285 GAGATCGCGGTACTTCGCAGAAATCAGCCATCCCAACATTGTGGCTCTGGAGGACGTCCAT 344  
|||||  
Db 61 GluIleAlaValLeuArgArgIleSerHisProAsnIleValAlaLeuGluAspValHis 80  
  
QY 345 GAGAGTCTCTCATCTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAACCTGTTTGAC 404  
|||||  
Db 81 GluSerProSerHisLeuTyrLeuAlaMetGluLeuValThrGlyGlyGluLeuPheAsp 100  
  
QY 405 CGCATATGGAGCGGGGCTCTACACAGAGAAGGACGCCAGCCACTGTAGGGCAGGTC 464  
|||||  
Db 101 ArgIleMetGluArgGlySerTyrThrGluLysAspAlaSerHisLeuValGlyGlnVal 120  
  
QY 465 CTGGCGCTGTCTCTACCTTCATAGCTGGGCATCGTGACCCGGGACCTCAAGCCTGAA 524  
|||||  
Db 121 LeuGlyAlaValSerTyrLeuHisSerLeuGlyIleValHisArgAspLeuLysProGlu 140  
  
QY 525 AACCTCTCTATGCCACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTGGCCTG 584  
|||||  
Db 141 AsnLeuLeuTyrAlaThrProPheGluAspSerLysIleMetValSerAspPheGlyLeu 160  
  
QY 585 TCCAAATACAAGCTGGCAACATGTAGGCACAGCCTGTGGGACCCAGGATATGTGGCC 644  
|||||  
Db 161 SerLysIleGlnAlaGlyAsnMetLeuGlyThrAlaCysGlyThrProGlyTyrValAla 180  
  
QY 645 CCAGAGCTCCTGGAGCAGAAACCTTACGGGAAGGCCGTAGATGTGGGCCCTGGGTGTC 704  
|||||  
Db 181 ProGluLeuLeuGluGlnLysProTyrGlyLysAlaValAspValTrpAlaLeuGlyVal 200  
  
QY 705 ATCTCCTACATCTGCTGTGTGGTACCCCTTCTATGATGAGACGGATCCTGAATC 764  
|||||  
Db 201 IleSerTyrIleLeuLeuCysGlyTyrProPheTyrAspGluSerAspProGluLeu 220  
  
QY 765 TTCAGCCAGATTCTGAGGGCCAGCTATGAGTTTGACTCCCTTTTGGGATGACATCTCA 824  
|||||  
Db 221 PheSerGlnIleLeuArgAlaSerTyrGluPheAspSerProPheTrpGlyAspIleSer 240  
  
QY 825 GAATCAGCCAAAGACTTCATTCCGCCACCTTCTGGAACGTGATCCCGAAGAGGTTTACC 884  
|||||  
Db 241 GluSerAlaLysAspPheIleArgHisLeuLeuGluArgAspProGlnLysArgPheThr 260  
  
QY 885 TGCCAGCAGGCCTACAGCATCTTTGGATCTCTGGGGATGCAGCCTTCGATAGGGACATC 944  
|||||  
Db 261 CysGlnGlnAlaLeuArgHisLeuTrpValSerGlyAspThrAlaPheAspArgAspIle 280  
  
QY 945 CTGGGTTCTGTGAGTCAGATCCAGAGAATTTTGGCAGGACCCACTGGAAGCGTGCA 1004  
|||||

Db 281 LeuGlySerValSerGluGlnIleArgLysAsnPheAlaArgThrHisTrpLysArgAla 300  
  
QY 1005 TTCAATGCCACATCATTTCTTACCTACATCCGTAAAGCTGGGACAAAGCCAGAGGTGAG 1064  
|||||  
Db 301 PheAsnAlaThrSerPheLeuArgHisIleArgLysLeuGlyGlnIleProGluGlyGlu 320  
  
QY 1065 GAGGCTCCAGGCAGTGTATGACCCGTCATAGCCACCCAGGCCCTGGGACTAGCCAGTCC 1124  
|||||  
Db 321 GlyAlaSerGluGlnGlyMetAlaArgHisSerHisSerGlyLeuArgAlaGlyGlnPro 340  
  
QY 1125 CCCAAGTGG 1133  
|||||  
Db 341 ProLysTrp 343  
  
RESULT 3  
ABP69106  
ID ABP69106 standard; protein; 372 AA.  
XX  
AC ABP69106;  
XX  
DT 20-JAN-2003 (first entry)  
XX  
DE Human polypeptide SEQ ID NO 1153.  
XX  
KW Human; genome mapping; gene therapy; food supplement; virus; fungus;  
cell-proliferative disorder; neurodegenerative disease; bacterial;  
Parkinson's disease; Alzheimer's disease; autoimmune disease;  
multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;  
arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;  
antiparkinsonian; antidiabetic; immunosuppressive; dermatological;  
haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;  
antiarthritic.  
XX  
OS Homo sapiens.  
XX  
PN WO200270539-A2.  
XX  
PD 12-SEP-2002.  
XX  
PF 05-MAR-2002; 2002WO-US005095.  
XX  
PR 05-MAR-2001; 2001US-00799451.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;  
Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;  
Wehrman T, Wang J, Wang D, Drmanac RT;  
XX  
DR WPI; 2002-759812/82.  
DR N-PSDB; ABZ11323.  
XX  
PT New polynucleotides comprising sequences assembled from expressed  
sequence tags (ESTs), useful for treating cell-proliferative,  
neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet  
or coagulation disorders.  
PS  
XX  
XX  
CC The invention relates to an isolated polynucleotide (I) comprising a  
nucleotide sequence selected from any of 948 sequences (ABZ11119-  
ABZ12066) or their mature protein coding portion, active domain coding  
protein or complementary sequences. The polynucleotides are useful for  
identifying expressed genes or for physical mapping of human genome. The  
encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight  
markers, as a food supplement, for generating antibodies, in medical  
imaging, screening and diagnostic assays and for treating cell-  
proliferative disorders (cancer), neurodegenerative diseases (Parkinson's  
or Alzheimer's disease), autoimmune diseases (multiple sclerosis,  
diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,  
platelet or coagulation disorders, wound, burns, incision, ulcers, liver  
or lung fibrosis, infections (bacterial, viral, fungal, parasitic),  
arthritis, etc. Note: The sequence data for this patent did not form part



CC of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX SQ Sequence 372 AA;

Alignment Scores:  
Pred. No.: 3.54e-130 Length: 372  
Score: 1673.50 Matches: 327  
Percent Similarity: 88.98% Conservative: 4  
Best Local Similarity: 87.90% Mismatches: 12  
Query Match: 58.27% Indels: 29  
DB: 5 Gaps: 1

US-10-032-254A-1 (1-1554) x ABP69106 (1-372)

QY	105	ATGCTGCTGCTCAAGAAACAGACGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAAG	164
Db	1	MetLeuLeuLeuLysHisThrGluAspIleSerSerValTyrGluIleArgGluArg	20
QY	165	CTGGGCTCG-----	173
Db	21	LeuGlySerGlyProSerProLeuHisSerLeuSerLeuLeuProLeuLeuSerSerHis	40
QY	174	-----GGTGCCTCTCTGAGGTGATGCTG	197
Db	41	PheLeuProThrSerHisArgProValCysGlyArgGlyAlaPheSerGluValValLeu	60
QY	198	GCCAGGAAAGGGCTCTGCTCATCTTGTGGCCCTCAAGTGCATTCCCAAGAAAGCACTT	257
Db	61	AlaGlnGluArgGlySerAlaHisLeuValAlaLeuLysCysIleProLysLysAlaLeu	80
QY	258	CGGGCAAGGAGGCCCTGGTGGAGAATGAGATCGCGGTACTTCGCAGAATCAGCCATCCC	317
Db	81	ArgGlyLysGluAlaLeuValGluAsnGluIleAlaValLeuArgArgIleSerHisPro	100
QY	318	AACATTGTGGCTCTGGAGGACGTCCATGAGAGTCTTCTCATCTCTACTTGGCCATGGAG	377
Db	101	AsnIleValAlaLeuGluAspValHisGluSerProSerHisLeuTyrLeuAlaMetGlu	120
QY	378	CTGGTAACAGGTGGTGAACCTTTTGACCGCATCATGGAGCGGGCTCCTACACAGAGAAG	437
Db	121	LeuValThrGlyGlyGluLeuPheAspArgIleMetGluArgGlySerTyrThrGluLys	140
QY	438	GACGCAGCCACCTTGTAGGGCAGGTCTTGGCGTGTCTCCTACCTTCATAGCCTGGSC	497
Db	141	AspAlaSerHisLeuValGlyGlnValLeuGlyAlaValSerTyrLeuHisSerLeuGly	160
QY	498	ATCGTGCAACGGGACCTCAAGCCTGAAACCTCCTCTATGCCACACACCTTTTGAGGACTCC	557
Db	161	IleValHisArgAspLeuLysProGluAsnLeuLeuTyrAlaThrProPheGluAspSer	180
QY	558	AAGATCATGGTCTCTGACTTTGGCCTGTCCAAATACAAGTCGGCAACATGCTAGGCACA	617
Db	181	LysIleMetValSerAspPheGlyLeuSerLysIleGlnAlaGlyAsnMetLeuGlyThr	200
QY	618	GCCTGTGGGACCCAGGATATGTGGCCCCCAGAGCTCCTGGAGCAGAAACCCCTACGGGAAG	677
Db	201	AlaCysGlyThrProGlyTyrValAlaProGluLeuLeuGluGlnLysProTyrGlyLys	220
QY	678	GCCGTAGATGTGTGGCCCTGGGTGTCATCTCCTACATCCTGCTGTGTGGGTACCCCCC	737
Db	221	AlaValAspValTrpAlaLeuGlyValIleSerTyrIleLeuLeuCysGlyTyrProPro	240
QY	738	TTCTATGATGAGCGCATCCTGAACCTTTCAGCCAGATTCTGAGGGCCAGCTATGATT	797
Db	241	PheTyrAspGluSerAspProGluLeuPheSerGlnIleLeuArgAlaSerTyrGluPhe	260
QY	798	GACTCCCCCTTTGGGATGACATCTCAGAATCAGCCAAAGACTTCATTGCCCCACCTTCIG	857
Db	261	AspSerProPheTrpAspAspIleSerGluSerAlaLysAspPheIleArgHisLeuLeu	280
QY	858	GAACGTGATCCCCAGAGAGGTTACCTGCCAGCAGGCCCTACAGCATCTTTGGATCTCT	917

Db	281	GluArgAspProGlnLysArgPheThrCysGlnGlnAlaLeuArgHisLeuTrpIleSer	300
QY	918	GGGATGCAGCCCTTCGATAGGACATCCTGGGTTCTGTCTCAGTGAGCAGATCCAGAAGAAT	977
Db	301	GlyAspThrAlaPheAspArgAspIleLeuGlySerValSerGluGlnIleArgLysAsn	320
QY	978	TTTGCCAGGACCCACTGGAAGCGTGCATTCAATGCCACATCATTCCTACGTCACATCCGT	1037
Db	321	PheAlaArgThrHisTrpLysArgAlaPheAsnAlaThrSerPheLeuArgHisIleArg	340
QY	1038	AAGCTGGGACAAAGCCAGAGGGTGAGGAGGCCTCCAGGCAGTGTATGACCCGTATAGC	1097
Db	341	LysLeuGlyGlnIleProGluGlyGluGlyAlaSerGluGlnGlyMetAlaArgHisSer	360
QY	1098	CACCCAGGCCTTGGGACTAGCCAGTCCCCCAAGTGG	1133
Db	361	HisSerGlyLeuArgAlaGlyGlnProProLysTrp	372
RESULT 4			
ID	ADR39752	standard; protein; 372 AA.	
XX	ADR39752;		
AC	ADR39752;		
XX	18-NOV-2004	(first entry)	
DT	18-NOV-2004	(first entry)	
XX	Human kinase and phosphatase KPP-25	protein SEQ ID NO:25.	
DE	human; kinase and phosphatase protein; KPP; enzyme; cytostatic;		
KW	antiarteriosclerotic; anticonvulsant; nootropic; neuroprotective;		
KW	cerebroprotective; anti-HIV; antiallergic; antiinflammatory;		
KW	thyromimetic; gene therapy; cell proliferative disorder; cancer;		
KW	atherosclerosis; neurological disorder; epilepsy; Huntington's disease;		
KW	stroke; immune disorder; inflammatory disorder; AIDS; allergy;		
KW	developmental disorder; Hypothyroidism; Cushing's syndrome; infection;		
KW	KPP-25.		
XX	Homo sapiens.		
OS	WO2004074453-A2.		
XX	02-SEP-2004.		
PF	20-FEB-2004; 2004WO-US0005092.		
XX	20-FEB-2003; 2003US-0449059P.		
PR	19-MAR-2003; 2003US-0456932P.		
PR	28-MAR-2003; 2003US-0458844P.		
PR	09-APR-2003; 2003US-0461678P.		
PR	17-APR-2003; 2003US-0463937P.		
XX	(INCY-) INCYTE CORP.		
PA	Ramkumar J, Marquis JP, Swarnakar A, Chawla NK, Tran UK;		
XX	Becha SD, Lee SY, Hafalia AJA, Richardson TW, Khare R, Jiang X;		
PI	Jackson AA, Yang J, Gorvad AE;		
PI	WPI; 2004-635568/61.		
DR	N-PSDB; ADR39798.		
XX	New human kinases and phosphatases (KPP) for diagnosing, treating and		
PT	preventing diseases or conditions associated with aberrant KPP expression		
PT	e.g. cancer, acquired immunodeficiency syndrome, epilepsy, or infections.		
XX	Claim 1; SEQ ID NO 25; 299pp; English.		
XX	The present sequence represents the human kinase and phosphatase protein		
CC	(KPP), designated KPP-25. The human KPP sequences from the present		
CC	invention have cytostatic, antiarteriosclerotic, anticonvulsant,		
CC	nootropic, neuroprotective, cerebroprotective, anti-HIV, antiallergic,		
CC	antiinflammatory and thyromimetic activities, and can be used in gene		
CC	therapy. The human KPP proteins and polynucleotides can be used in		
CC	diagnosing, treating and preventing diseases or conditions associated		



CC with the decreased expression or overexpression of KPP, such as cell  
CC proliferative (e.g. cancer, atherosclerosis), neurological (e.g.  
CC epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS,  
CC allergies) and developmental (e.g. Hypothyroidism, Cushing's syndrome)  
CC disorders, or infections. They can also be used in assessing the effects  
CC of exogenous compounds on the expression of nucleic acid and amino acid  
CC sequences of KPP. The KPP or its fragments are useful in screening  
CC compounds for effectiveness as agonist or antagonist of the polypeptides,  
CC or in altering the expression of the target polynucleotide and compounds  
CC that specifically bind to or modulate the activity of the polypeptide.

SQ Sequence 372 AA;

Alignment Scores:  
Pred. No.: 3.54e-130 Length: 372  
Score: 1673.50 Matches: 327  
Percent Similarity: 88.98% Conservative: 4  
Best Local Similarity: 87.90% Mismatches: 12  
Query Match: 58.27% Indels: 29  
DB: 8 Gaps: 1

US-10-032-254A-1 (1-1554) x ADR39752 (1-372)

QY 105 ATGCTGCTGCTCAAGAAACAGACGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAAG 164  
|||||  
Db 1 MetLeuLeuLeuLysHisThrGluAspIleSerSerValTyrGluIleArgGluArg 20  
QY 165 CTGGGCTCG----- 173  
|||||  
Db 21 LeuGlySerGlyProSerProLeuHisSerLeuSerLeuLeuProLeuLeuSerSerHis 40  
QY 174 -----GGTGCCTTCTCTGAGGTGATGCTG 197  
|||||  
Db 41 PheLeuProThrSerHisArgProValCysGlyArgGlyAlaPheSerGluValValLeu 60  
QY 198 GCCCAGGAAAGGGCTCTGCTCATCTTGTGGCCCTCAAGTGCATTCCCAAGAAAGCACTT 257  
|||||  
Db 61 AlaGlnGluArgGlySerAlaHisLeuValAlaLeuLysCysIleProLysLysAlaLeu 80  
QY 258 CGGGCAAGGAGGCCCTGGTGGAATGAGATCGCGGTACTTCGAGAATCAGCCATCCC 317  
|||||  
Db 81 ArgGlyLysGluAlaLeuValGluAsnGluIleAlaValLeuArgArgIleSerHisPro 100  
QY 318 AACATTGTGGCTCTGGAGGACGTCATGAGAGTCCTTCTCATCTCTACTTGGCCATGGAG 377  
|||||  
Db 101 AsnIleValAlaLeuGluAspValHisGluSerProSerHisLeuTyrLeuAlaMetGlu 120  
QY 378 CTGTTAACAGGTGGTGAACCTGTTTACCGCATCATGGAGCGGGCTCCTACACAGAGAAG 437  
|||||  
Db 121 LeuValThrGlyGlyGluLeuPheAspArgIleMetGluArgGlySerTyrThrGluLys 140  
QY 438 GACGCAGCCACCTTGTAGGCGAGGTCCTTGGCGTGTCTCTACCTTCATAGCCTGGGC 497  
|||||  
Db 141 AspAlaSerHisLeuValGlyGlnValLeuGlyAlaValSerTyrLeuHisSerLeuGly 160  
QY 498 ATCGTGCAACGGGACCTCAAGCCTGAAACCTCCTCTATGCCACACCTTTTGAGGACTCC 557  
|||||  
Db 161 IleValHisArgAspLeuLysProGluAsnLeuLeuTyrAlaThrProPheGluAspSer 180  
QY 558 AAGATCATGGTCTCTGACTTTGGCCCTGTCTCCAAAATACAAGCTGGCAACATGTCAGGCACA 617  
|||||  
Db 181 LysIleMetValSerAspPheGlyLeuSerLysIleGlnAlaGlyAsnMetLeuGlyThr 200  
QY 618 GCCTGTGGGACCCAGGATATGTGGCCCGCAGAGCTCCTGGAGCAGAAACCTTACGGGAAG 677  
|||||  
Db 201 AlaCysGlyThrProGlyTyrValAlaProGluLeuLeuGluGlnLysProTyrGlyLys 220  
QY 678 GCCGTAGATGTGTGGCCCTGGGTGTCTATCTCCTACATCCTGTGTGTGGGTACCCCCC 737  
|||||  
Db 221 AlaValAspValTrpAlaLeuGlyValIleSerTyrIleLeuLeuCysGlyTyrProPro 240  
QY 738 TTCTATGATGAGAGCGGATCCTGAACCTTTCAGCCAGATTCTGAGGCCAGCTATGAGTTT 797  
|||||

Db 241 PheTyrAspGluSerAspProGluLeuPheSerGlnIleLeuArgAlaSerTyrGluPhe 260  
QY 798 GACTCCCCCTTTGGGATGACATCTCAGAAATCAGCCAAAGACTTCATTGCGCCACCTTCTG 857  
|||||  
Db 261 AspSerProPheTrpAspIleSerGluSerAlaLysAspPheIleArgHisLeuLeu 280  
QY 858 GAACGTGATCCCCAGAAAGGTTACCTGCCAGCAGGCCCTACAGCATCTTTGGATCTCT 917  
|||||  
Db 281 GluArgAspProGlnLysArgPheThrCysGlnGlnAlaLeuArgHisLeuTrpIleSer 300  
QY 918 GGGATGCAGCCTTCGATAGGACATCCTGGGTTCTGTCAAGTCAAGATCCAGAAGAAT 977  
|||||  
Db 301 GlyAspThrAlaPheAspArgAspIleLeuGlySerValSerGluGlnIleArgLysAsn 320  
QY 978 TTTGCCAGGACCCACTGGAAGCGTGCATTCAATGCCACATCATCTCCTACGTCAACATCCGT 1037  
|||||  
Db 321 PheAlaArgThrHisTrpLysArgAlaPheAsnAlaThrSerPheLeuArgHisIleArg 340  
QY 1038 AAGCTGGGACAAAGCCAGAGSGTGAGGAGGCCCTCCAGGCGAGTGTATGACCCGTATAGC 1097  
|||||  
Db 341 LysLeuGlyGlnIleProGluGlyGluGlyAlaSerGluGlnGlyMetAlaArgHisSer 360  
QY 1098 CACCAGGCCCTTGGGACTAGCCAGTCCCCCAAGTGG 1133  
|||||  
Db 361 HisSerGlyLeuArgAlaGlyGlnProProLysTrp 372  
RESULT 5  
AAW88436  
ID AAW88436 standard; protein; 343 AA.  
XX AC AAW88436;  
XX DT 26-APR-1999 (first entry)  
XX DE Disease associated protein kinase DAPK-5.  
XX KW DAPK-5; disease associated protein kinase; human; diagnosis; therapy;  
KW adult respiratory distress syndrome; allergy; asthma; arteriosclerosis;  
KW bronchitis; emphysema; hypereosinophilia; myocardial inflammation;  
KW pericardial inflammation; anaemia; rheumatoid arthritis;  
KW Addison's disease; AIDS; atherosclerosis; atopic dermatitis;  
KW dermatomyositis; diabetes mellitus; glomerulonephritis; gout;  
KW Grave's disease; lupus erythematosus; multiple sclerosis;  
KW myasthenia gravis; osteoarthritis; osteoporosis; pancreatitis;  
KW polycystic kidney disease; polymyositis; scleroderma;  
KW Sjorgren's syndrome; autoimmune thyroiditis; cancer; infection; trauma;  
KW cell proliferation.  
XX OS Homo sapiens.  
XX FH Key Location/Qualifiers  
FT Binding-site 22. .294  
FT Peptide /note= "potential ATP binding site"  
FT /note= "catalytic loop"  
FT Modified-site 171  
FT Misc-difference 233 /note= "putative phosphorylation site"  
FT /note= "encoded by TNT"  
FT Misc-difference 328 /note= "encoded by GSC"  
FT Misc-difference 329 /note= "encoded by CGN"  
FT Misc-difference 333 /note= "encoded by TNA"  
XX WO9858052-A2.  
XX 23-DEC-1998.  
XX 19-JUN-1998; 98WO-US012813.  
XX 19-JUN-1997; 97US-00878989.  
PR

XX (INCY-) INCYTE PHARM INC.  
PA Bandman O, Hillman JL, Corley NC, Guegler KJ, Lal P, Goli SK;  
XX Shah P;  
PI WPI; 1999-080952/07.  
XX N-PSDB; AAX06835.  
DR New disease associated protein kinases - used to stimulate cell  
DR proliferation and to treat the immune response and cancer.  
XX Claim 1; Page 59-60; 93pp; English.  
PS This is the amino acid sequence of human disease associated protein  
XX kinase DAPK-5, as deduced from a consensus sequence (see AAX06835) of  
CC overlapping cDNA clones from libraries which are immortalised or  
CC cancerous. DAPK-5 shows 64% homology to human Cam-kinase, CamKI (GI  
CC 790790). The invention provides DAPK-1 to DAPK-7 polypeptides (see  
CC AAW88432-38) and cDNA clones encoding them (see AAX06831-36 and  
CC AAX06882), as well as expression vectors, host cells, agonists,  
CC antagonists and antibodies. The invention further provides uses of such  
CC products in the diagnosis, prevention and treatment of diseases  
CC associated with cell proliferation, especially cancer or an immune  
CC response (claimed). Conditions that may be treated include adult  
CC respiratory distress syndrome, allergies, asthma, arteriosclerosis,  
CC bronchitis, emphysema, hypereosinophilia, myocardial or pericardial  
CC inflammation, rheumatoid arthritis, Addison's disease, AIDS, anaemia,  
CC atherosclerosis, various diseases of the digestive system, atopic  
CC dermatitis, dermatomyositis, diabetes mellitus, glomerulonephritis, gout,  
CC Grave's disease, lupus erythematosus, multiple sclerosis, myasthenia  
CC gravis, osteoarthritis, osteoporosis, pancreatitis, polycystic kidney  
CC disease, polymyositis, scleroderma, Sjorgren's syndrome, autoimmune  
CC thyroiditis, complications of cancer, extracorporeal circulation, viral,  
CC bacterial, fungal, parasitic, protozoal and helminthic infections, and  
CC trauma (disclosed)  
XX  
SQ Sequence 343 AA;  
  
Alignment Scores:  
Pred. No.: 3.73e-126 Length: 343  
Score: 1625.00 Matches: 316  
Percent Similarity: 93.29% Conservative: 4  
Best Local Similarity: 92.13% Mismatches: 23  
Query Match: 56.58% Indels: 0  
DB: 2 Gaps: 0  
  
US-10-032-254A-1 (1-1554) x AAW88436 (1-343)  
  
QY 105 ATGCTGCTGCTCAAGAAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAAG 164  
Db 1 MetLeuLeuLeuLysLysHisThrGluAspIleSerSerValTyrGluIleArgGluArg 20  
  
QY 165 CTGGGCTCGGGTGCCTTCTCTGAGGTGATGCTGGCCAGGAAAGGGGCTCTGCTCATCTT 224  
Db 21 LeuGlySerGlyAlaPheSerGluValValLeuAlaGlnGluArgGlySerAlaHisLeu 40  
  
QY 225 GTGGCCCTCAAGTGCATTCCCAAGAAAGCACTTCGGGGCAAGGAGGCCCTGGTGGAGAAT 284  
Db 41 ValAlaLeuLysCysIleProLysLysAlaLeuArgGlyLysGluAlaLeuValGluAsn 60  
  
QY 285 GAGATCGCGGTACTTCGCAGAATCAGGCATCCCAACATTGTGGTCTGGAGGACGTCCAT 344  
Db 61 GluIleAlaValLeuArgArgIleSerHisProAsnIleValAlaLeuGluAspValHis 80  
  
QY 345 GAGATCCTTCTCATCTCTACTTGGCCATGGAGCTGGTAACAGTGGTGAACCTGTTTGAC 404  
Db 81 GluSerProSerHisLeuTyrLeuAlaMetGluLeuValThrGlyGlyGluLeuPheAsp 100  
  
QY 405 CGCATCATGGAGCGGGGCTCCTACACAGAGAAGGACGCCACCTTGTAGGGCAGGTC 464  
Db 101 ArgIleMetGluArgGlySerTyrThrGluLysAspAlaSerHisLeuValGlyGlnVal 120

QY 465 CTTGGCGCTGTCTCTACCTTCATAGCCCTGGGCATCGTCACCGGACCTCAAGCCTGAA 524  
Db 121 LeuGlyAlaValSerTyrLeuHisSerLeuGlyIleValHisArgAspLeuLysProGlu 140  
  
QY 525 AACCTCCTCTATATGCCACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTGGCCTG 584  
Db 141 AsnLeuLeuTyrAlaThrPropheGluAspSerLysIleMetValSerAspPheGlyLeu 160  
  
QY 585 TCCAAAATACAAGCTGGCAACATGCTAGGCACAGCCCTGTGGGACCCCAGGATATGTGGCC 644  
Db 161 SerLysIleGlnAlaGlyAsnMetLeuGlyThrAlaCysGlyThrProGlyTyrvalAla 180  
  
QY 645 CCAGAGCTCTGGAGCAGAAACCTTACGGGAAGGCCGTAGATGTGTGGCCCTGGGTGTC 704  
Db 181 ProGluLeuLeuGluGlnLysProTyrGlyLysAlaValAspValTrpAlaLeuGlyVal 200  
  
QY 705 ATCTCCTACATCCTGCTGTGTGGGTACCCCCCTTCTATGATGAGAGCGATCCTGAATC 764  
Db 201 IleSerTyrIleLeuLeuCysGlyTyrProProPheTyrAspGluSerAspProGluLeu 220  
  
QY 765 TTCAGCCAGATTCTGAGSGCCAGCTATGAGTTTGACTCCCCCTTTTGGGATGACATCTCA 824  
Db 221 PheSerGlnIleLeuArgAlaSerTyrGluPheAsp\*\*\*ProPheTrpAspAspIleSer 240  
  
QY 825 GAATCAGCCAAAGACTTCATTTCGCCACCTTCTTGGAACTGATCCCCAGAGAGTTCCACC 884  
Db 241 GluSerGlyLysAspPheIleArgHisLeuLeuGluArgAspLeuGlnLysArgPheThr 260  
  
QY 885 TGCCAGCAGGCCCTACAGCATCTTTGGATCTCTGGGGATGTCAGCCCTTCGATAGGGACATC 944  
Db 261 CysGlnGlnAlaLeuArgAspLeuTrpIlePheTrpAspThrGlyPheGlyArgAspIle 280  
  
QY 945 CTGGGTCTGTGAGTGAGCAGATCCAGAAGAATTTTGCAGGACCCACTGGAAGCGTGCA 1004  
Db 281 LeuGlyPheValSerGluGlnIleArgLysAsnPheAlaTrpThrHisTrpLysArgAla 300  
  
QY 1005 TTCAATGCCACATCATTCCTACGTCACATCCGTAAGCTGGGACAAAGCCAGAGGGTGAG 1064  
Db 301 PheAsnAlaThrLeuPheLeuArgHisIleArgLysLeuGlyGlnIleProGluGlyGlu 320  
  
QY 1065 GAGGCCTCCAGGCAGTGTATGACCCCGTCATAGCCACCCAGGCCCTTGGGACTAGCCAGTCC 1124  
Db 321 GlyAlaSerGluGlnGlyMet\*\*\*ArgHisSerHis\*\*\*GlyLeuArgAlaGlyGlnPro 340  
  
QY 1125 CCCAAGTGG 1133  
Db 341 ProLysTrp 343  
  
RESULT 6  
ADL06509  
ID ADL06509 standard; protein; 343 AA.  
XX  
AC ADL06509;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Human tumour-associated antigenic target (TAT) polypeptide #8.  
XX  
KW Human; tumour-associated antigenic target; TAT; cell death; tumour;  
KW cancer; cytostatic.  
XX  
OS Homo sapiens.  
XX  
PN WO2004016225-A2.  
XX  
PD 26-FEB-2004.  
XX  
PF 19-AUG-2003; 2003WO-US025892.  
XX  
PR 19-AUG-2002; 2002US-0404809P.  
PR 21-AUG-2002; 2002US-0405645P.  
PR 23-SEP-2002; 2002US-0413192P.  
PR 15-OCT-2002; 2002US-0419008P.

PR 15-NOV-2002; 2002US-0426847P.  
PR 02-JUL-2003; 2003US-0484959P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Desauvage FJ, Frantz G, Hillan KJ, Polakis P, Polson A, Smith V;  
PI Spencer SD, Wu TD, Zhang Z;  
XX  
DR WPI; 2004-257144/24.  
DR N-PSDB; ADL06429.  
XX  
PT New antibody that binds to a tumor-associated antigenic target (TAT)  
PT polypeptide, useful for preparing a composition for diagnosing or  
PT treating cancer.  
XX  
PS Claim 2; SEQ ID NO 89; 319pp; English.  
XX  
CC The present invention relates to the isolation of human tumour-associated  
CC antigenic target (TAT) polynucleotide and polypeptide sequences. Also  
CC disclosed is an antibody that binds to a TAT polypeptide. The antibody is  
CC a monoclonal antibody, an antibody fragment, a chimeric antibody or a  
CC humanised antibody. It is conjugated to a growth inhibitory agent. It is  
CC produced in bacteria or in CHO cells and induces death of a cell to which  
CC it binds. The antibody is useful for preparing a composition for  
CC diagnosing or treating tumours and cancer. The present sequence  
CC represents a human TAT polypeptide of the invention.  
XX  
SQ Sequence 343 AA;  
  
Alignment Scores:  
Pred. No.: 3.73e-126 Length: 343  
Score: 1625.00 Matches: 316  
Percent Similarity: 93.29% Conservative: 4  
Best Local Similarity: 92.13% Mismatches: 23  
Query Match: 56.58% Indels: 0  
DB: 8 Gaps: 0  
  
US-10-032-254A-1 (1-1554) x ADL06509 (1-343)  
  
QY 105 ATGCTGCTCAAGAAACAGACGAGGAGACATCAGCAGTGTCTATGAGATCCGGGAGAAG 164  
DB 1 MetLeuLeuLeuLysHisThrGluAspIleSerSerValTyrGluIleArgGluArg 20  
  
QY 165 CTGGGCTCGGGTGCCTTCTCTGAGGTGATGCTGGCCAGGAAGGGGCTCTGCTCATCTT 224  
DB 21 LeuGlySerGlyAlaPheSerGluValValLeuAlaGlnGluArgGlySerAlaHisLeu 40  
  
QY 225 GTGGCCCTCAAGTGCATTCCCAAGAAAGCACTTCGGGGCAAGAGGCCCTGGTGGAGAAT 284  
DB 41 ValAlaLeuLysCysIleProLysLysAlaLeuArgGlyLysGluAlaLeuValGluAsn 60  
  
QY 285 GAGATCGGGTACTTCGCAGAAATCAGCCATCCCAACATTGTGGCTCTGGAGGACGTCCAT 344  
DB 61 GluIleAlaValLeuArgArgIleSerHisProAsnIleValAlaLeuGluAspValHis 80  
  
QY 345 GAGAGTCTTCTCATCTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAACGTGTTGAC 404  
DB 81 GluSerProSerHisLeuTyrLeuAlaMetGluLeuValThrGlyGlyGluLeuPheAsp 100  
  
QY 405 CGCATCATGGAGCGGGGCTCCTACACAGAGAAGGACGCCACCTTGTAGGGCAGGTC 464  
DB 101 ArgIleMetGluArgGlySerTyrThrGluLysAspAlaSerHisLeuValGlyGlnVal 120  
  
QY 465 CTGGCGCTGTCTCTACCTTCTATAGCTGGGCATCGTGACCGGGACCTCAAGCCTGAA 524  
DB 121 LeuGlyAlaValSerTyrLeuHisSerLeuGlyIleValHisArgAspLeuLysProGlu 140  
  
QY 525 AACCTCCTCTATGCCACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTGGCCTG 584  
DB 141 AsnLeuLeuTyrAlaThrProPheGluAspSerLysIleMetValSerAspPheGlyLeu 160  
  
QY 585 TCCAAATACAAGCTGGCAACATGTAGGCACAGCCTGTGGGACCCAGGATATGTGGCC 644  
DB 141 AsnLeuLeuTyrAlaThrProPheGluAspSerLysIleMetValSerAspPheGlyLeu 160

Db 161 SerLysIleGlnAlaGlyAsnMetLeuGlyThrAlaCysGlyThrProGlyTyrValAla 180  
QY 645 CCAGAGCTCTGGAGCAGAAACCTACGGGAAGCCGTAGATGTGTGGGCCCTGGGTGTC 704  
Db 181 ProGluLeuLeuGluGlnLysProTyrGlyLysAlaValAspValTrpAlaLeuGlyVal 200  
QY 705 ATCTCTACATCCTGCTGTGTGGGTACCCCTTCTATGATGAGAGCGATCCTGAACTC 764  
Db 201 IleSerTyrIleLeuLeuCysGlyTyrProProPheTyrAspGluSerAspProGluLeu 220  
QY 765 TTCAGCCAGATTCTGAGGGCCAGCTATGAGTTTGACTCCCCCTTTTGGGATGACATCTCA 824  
Db 221 PheSerGlnIleLeuArgAlaSerTyrGluPheAsp\*\*\*ProPheTrpAspAspIleSer 240  
QY 825 GAATCAGCCAAAGACTTCATTCCGCCACCTTCTTGGAAACGTGATCCCCAGAAAGAGTTTCACC 884  
Db 241 GluSerGlyLysAspPheIleArgHisLeuLeuGluArgAspLeuGlnLysArgPheThr 260  
QY 885 TGCCAGCAGGCCCTACAGCATCTTTGGATCTCTGGGGATGCAGCCTTCGATAGGGACATC 944  
Db 261 CysGlnGlnAlaLeuArgAspLeuTrpIlePheTrpAspThrGlyPheGlyArgAspIle 280  
QY 945 CTGGGTCTGTCTCAGTGAGCAGATCCAGAAAGAAATTTGCCAGGACCCACTGGAAAGCGTGCA 1004  
Db 281 LeuGlyPheValSerGluGlnIleArgLysAsnPheAlaTrpThrHisTrpLysArgAla 300  
QY 1005 TTCAATGCCACATCATTTCTACGTCACATCCGTAAGCTGGGACAAAGCCAGAGGTGAG 1064  
Db 301 PheAsnAlaThrLeuPheLeuArgHisIleArgLysLeuGlyGlnIleProGluGlyGlu 320  
QY 1065 GAGGCCTCCAGGCAGTGTATGACCCGTATAGCCATAGCCACCCAGGCCTTGGGACTAGCCAGTCC 1124  
Db 321 GlyAlaSerGluGlnGlyMet\*\*\*ArgHisSerHis\*\*\*GlyLeuArgAlaGlyGlnPro 340  
QY 1125 CCCAAGTGG 1133  
Db 341 ProLysTrp 343  
  
RESULT 7  
ADM72655  
ID ADM72655 standard; protein; 343 AA.  
XX  
AC ADM72655;  
XX  
DT 17-JUN-2004 (first entry)  
XX  
DE Human TASK120 polypeptide (clone DNA151475).  
XX  
KW TASK; tumour-associated kinase; cytostatic; tumour;  
KW cell proliferative disorder; cancer; transgenic;  
KW chromosome identification; tissue typing; human; TASK120; enzyme.  
XX Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 233 /note= "encoded by TNT"  
FT Misc-difference 328 /note= "encoded by GSC"  
FT Misc-difference 333 /note= "encoded by TNA"  
XX  
PN WO2004024063-A2.  
XX  
PD 25-MAR-2004.  
XX  
PF 05-SEP-2003; 2003WO-US027886.  
XX  
PR 11-SEP-2002; 2002US-0410166P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Davis DP, Desauvage FJ, Wood WI, Zhang Z;



XX WPI; 2004-282984/26.  
DR N-PSDB; ADM72654.  
XX  
PT New tumor-associated kinase nucleic acids and polypeptides, useful as  
PT hybridization probes for isolating full length TASK DNA, for generating  
PT transgenic animals, in chromosome identification, or for tissue typing.  
XX  
PS Claim 11; Fig 6; 140pp; English.  
XX  
CC The invention relates to tumour-associated kinase (TASK) polypeptides  
CC (II) and encoding polynucleotides. An antibody, oligopeptide (siRNA) or  
CC organic molecule that binds to (II) is useful for treating a mammal  
CC having a tumour comprising cells expressing (II). Antagonists of TASK are  
CC useful for treating or preventing a cell proliferative disorder (e.g.  
CC cancer) associated with increased expression or activity of (II). The  
CC TASK polynucleotides and polypeptides may be used as hybridization probes  
CC for isolating full length TASK DNA, for generating transgenic animals, in  
CC chromosome identification, or for tissue typing. The present sequence  
CC represents a human TASK120 polypeptide.  
XX  
SQ Sequence 343 AA;

Alignment Scores:  
Pred. No.: 3.73e-126 Length: 343  
Score: 1625.00 Matches: 316  
Percent Similarity: 93.29% Conservative: 4  
Best Local Similarity: 92.13% Mismatches: 23  
Query Match: 56.58% Indels: 0  
DB: 8 Gaps: 0

US-10-032-254A-1 (1-1554) x ADM72655 (1-343)

QY 105 ATGCTGCTGCTCAAGAAACAGACGGAGACATCAGCAGTGTCTATGAGATCCGGGAGAAG 164  
Db 1 MetLeuLeuLeuLysLysHisThrGluAspIleSerSerValTyrGluIleArgGluArg 20  
QY 165 CTGGGCTCGGTCCTTCTCTGAGGTGATGCTGGCCAGGAAAGGGCTCTGCTCATCTT 224  
Db 21 LeuGlySerGlyAlaPheSerGluValValLeuAlaGlnGluArgGlySerAlaHisLeu 40  
QY 225 GTGGCCCTCAAGTGCATTCCCAAGAAACACACTTCGGGGCAAGGAGCCCTGGTGAGAAAT 284  
Db 41 ValAlaLeuLysCysIleProLysLysAlaLeuArgGlyLysGluAlaLeuValGluAsn 60  
QY 285 GAGATCGCGGTACTTCGCAGAAATCAGCCATCCCAACATTGTGGCTCTGGAGGACGTCCAT 344  
Db 61 GluIleAlaValLeuArgArgIleSerHisProasnIleValAlaLeuGluAspValHis 80  
QY 345 GAGAGTCCTTCTCATCTCTACTTGGCCATGGAGCTGGTAACAGTGGTGAACGTGTTGAC 404  
Db 81 GluSerProSerHisLeuTyrLeuAlaMetGluLeuValThrGlyGlyGluLeuPheAsp 100  
QY 405 CGCATCATGAGCGGGGCTCCTACACAGAGAAGGACGCCAGCCACTTGTAGGGCAGGTC 464  
Db 101 ArgIleMetGluArgGlySerTyrThrGluLysAspAlaSerHisLeuValGlyGlnVal 120  
QY 465 CTGGCGCTGTCTCTACCTTCATAGCCCTGGGCATCGTGCACCGGACCTCAAGCCTGAA 524  
Db 121 LeuGlyAlaValSerTyrLeuHisSerLeuGlyIleValHisArgAspLeuLysProGlu 140  
QY 525 AACCTCCTCTATGCCACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTGGCCTG 584  
Db 141 AsnLeuLeuTyrAlaThrProPheGluAspSerLysIleMetValSerAspPheGlyLeu 160  
QY 585 TCCAAATACAAGCTGGCAACATGCTAGGCACAGCCCTGTGGGACCCAGGATATGTGGCC 644  
Db 161 SerLysIleGlnAlaGlyAsnMetLeuGlyThrAlaCysGlyThrProGlyTyrValAla 180  
QY 645 CCAGAGCTCTGGAGCAGAAACCTACGGGAAGGCCGTAGATGTGGGCCCTGGGTGC 704  
Db 181 ProGluLeuLeuGluGlnLysProTyrGlyLysAlaValAspValTrpAlaLeuGlyVal 200

QY 705 ATCTCTACATCCTGTGTGGGTACCCCTTCTATGATGAGAGCGATCCTGAATC 764  
Db 201 IleSerTyrIleLeuLeuCysGlyTyrProProPheTyrAspGluSerAspProGluLeu 220  
QY 765 TTCAGCCAGATTCTGAGGGCCAGCTATGAGTTTGACTCCCTTTTGGGATGACATCTCA 824  
Db 221 PheSerGlnIleLeuArgAlaSerTyrGluPheAsp\*\*\*PropheTrpAspAspIleSer 240  
QY 825 GAATCAGCCAAAGACTTCATTGCGCCACCTTCTGGAACGTGATCCCCAGAAGAGTTTACC 884  
Db 241 GluSerGlyLysAspPheIleArgHisLeuLeuGluArgAspLeuGlnLysArgPheThr 260  
QY 885 TGCCAGCAGGCCCTACAGCATCTTTGGATCTCTGGGGATGCAGCCTTCGATAGGGACATC 944  
Db 261 CysGlnGlnAlaLeuArgAspLeuTrpIlePheTrpAspThrGlyPheGlyArgAspIle 280  
QY 945 CTGGGTCTGTGAGTGAGCAGATCCAGAAGAATTTTGCAGGACCCACTTGAAGCGTGCA 1004  
Db 281 LeuGlyPheValSerGluGlnIleArgLysAsnPheAlaTrpThrHisTrpLysArgAla 300  
QY 1005 TTCAATGCCACATCATCTCTACGTACATCCGTAAAGCTGGGACAAAGCCAGAGGTGAG 1064  
Db 301 PheAsnAlaThrLeuPheLeuArgHisIleArgLysLeuGlyGlnIleProGluGlyGlu 320  
QY 1065 GAGGCCTCCAGGCAGTGTATGACCCGTATAGCCACCCAGGCCCTTGGGACTAGCCAGTCC 1124  
Db 321 GlyAlaSerGluGlnGlyMet\*\*\*ArgHisSerHis\*\*\*GlyLeuArgAlaGlyGlnPro 340  
QY 1125 CCCAAGTGG 1133  
Db 341 ProLysTrp 343

RESULT 8  
ADM72237  
ID ADM72237 standard; protein; 343 AA.  
XX  
AC ADM72237;  
XX  
DT 17-JUN-2004 (first entry)  
XX  
DE Human TASK100 polypeptide.  
XX  
KW TASK; tumour-associated kinase; cytostatic; tumour antigen;  
KW cell proliferative disorder; cancer; transgenic; human.  
XX  
OS Homo sapiens.  
XX  
PN WO2004024064-A2.  
XX  
PD 25-MAR-2004.  
XX  
PF 05-SEP-2003; 2003WO-US027894.  
XX  
PR 11-SEP-2002; 2002US-0410166P.  
XX  
PA (GETH ) GENENTECH INC.  
XX  
PI Desauvage FJ, Wood WI, Zhang Z;  
XX  
DR WPI; 2004-282985/26.  
DR N-PSDB; ADM72236.  
XX  
PT New tumor-associated kinase nucleic acids and polypeptides, useful as  
PT hybridization probes for isolating full length TASK DNA, for generating  
PT transgenic animals, in chromosome identification, or for tissue typing.  
XX  
PS Claim 12; SEQ ID NO 42; 163pp; English.  
XX  
CC The invention relates to new isolated tumour-associated kinase (TASK)  
CC nucleic acid molecules and encoded polypeptides. Cytostatic. The  
CC antibody, oligopeptide or organic molecule that binds to the TASK  
CC polypeptide are useful for treating a mammal having a tumour comprising  
CC cells expressing the polypeptide. Antagonists of TASK are useful for

CC treating or preventing a cell proliferative disorder (e.g. cancer)  
CC associated with increased expression or activity of TASK polypeptide. The  
CC TASK polynucleotides and polypeptides may be used as hybridization probes  
CC for isolating full length TASK DNA, for generating transgenic animals, in  
CC· chromosome identification, or for tissue typing. The present sequence  
CC represents a human TASK polypeptide.  
XX  
SQ Sequence 343 AA;

Alignment Scores:  
Pred. No.: 3.73e-126 Length: 343  
Score: 1625.00 Matches: 316  
Percent Similarity: 93.29% Conservative: 4  
Best Local Similarity: 92.13% Mismatches: 23  
Query Match: 56.58% Indels: 0  
DB: 8 Gaps: 0

US-10-032-254A-1 (1-1554) x ADM72237 (1-343)

QY	105	ATGCTGCTGCTCAAGAAACAGACGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAG	164
Db	1	MetLeuLeuLeuLysHisThrGluAspIleSerSerValTyrGluIleArgGluArg	20
QY	165	CTGGCTCGGTGCTTCTCTGAGGTGATGCTGGCCAGGAAGGGCTCTGCTCATCTT	224
Db	21	LeuGlySerGlyAlaPheSerGluValValLeuAlaGlnGluArgGlySerAlaHisLeu	40
QY	225	GTGGCCTCAAGTGCATTCCCAAGAAAGCACCTTCGGGGCAAGAGGCCCTGGTGGAGAT	284
Db	41	ValAlaLeuLysCysIleProLysLysAlaLeuArgGlyLysGluAlaLeuValGluAsn	60
QY	285	GAGATCGCGTACTTTCGAGAAATCAGCCATCCCAACATTGTGGCTCTGGAGGACGTCCAT	344
Db	61	GlulieAlaValLeuArgArgIleSerHisProAsnIleValAlaLeuGluAspValHis	80
QY	345	GAGATCCTTCTCATCTCTACTTGGCCATGGAGCTGGTAACAGTGGTGAACCTGTTTAC	404
Db	81	GlusSerProSerHisLeuTyrLeuAlaMetGluLeuValThrGlyGlyGluLeuPheAsp	100
QY	405	CGCATCATGGAGCGGGCTCCTACACAGAGAAGGACGCCAGCCACCTTGTAGGGCAGGTC	464
Db	101	ArgIleMetGluArgGlySerTyrThrGluLysAspAlaSerHisLeuValGlyGlnVal	120
QY	465	CTTGGCGCTGTCTCCTACCTTCATAGCCTGGGCATCGTGCACCGGGACCTCAAGCCTGA	524
Db	121	LeuGlyAlaValSerTyrLeuHisSerLeuGlyIleValHisArgAspLeuLysProGlu	140
QY	525	AACCTCCTCTATGCCACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTGGCCTG	584
Db	141	AsnLeuLeuTyrAlaThrProPheGluAspSerLysIleMetValSerAspPheGlyLeu	160
QY	585	TCCAAATACAAGCTGGCAACATGCTAGGCACAGCCTGTGGGACCCAGGATATGTGGCC	644
Db	161	SerLysIleGlnAlaGlyAsnMetLeuGlyThrAlaCysGlyThrProGlyTyrValAla	180
QY	645	CCAGAGCTCTGGAGCAGAAACCCCTACGGGAAGCCGTAGATGTGTGGCCCTGGGTGTC	704
Db	181	ProGluLeuLeuGluGlnLysProTyrGlyLysAlaValAspValTrpAlaLeuGlyVal	200
QY	705	ATCTCCTACATCCTGTGTGTGGGTACCCCCCTTCTATGATGAGAGCGATCCTGAACTC	764
Db	201	IleSerTyrIleLeuLeuCysGlyTyrProProPheTyrAspGluSerAspProGluLeu	220
QY	765	TTCAGCCAGATTCTGAGGGCCAGCTATGAGTTTGACTCCCCCTTTGGGATGACATCTCA	824
Db	221	PheSerGlnIleLeuArgAlaSerTyrGluPheAsp**ProPheTrpAspIleSer	240
QY	825	GAATCAGCAAAAGACTTCATTCCGCACCTTCTGGAACGTGATCCCCAGAGAGGTTTCAAC	884
Db	241	GluSerGlyLysAspPheIleArgHisLeuLeuGluArgAspLeuGlnLysArgPheThr	260
QY	885	TGCCAGAGGCCCTACAGCATCTTTGGATCTCTGGGGATGCAGCCTTCGATAGGGACATC	944

Db	261	CysGlnGlnAlaLeuArgAspLeuTrpIlePheTrpAspThrGlyPheGlyArgAspIle	280
QY	945	CTGGGTTCTGTCAGTGAGCAGATCCAGAAGAAATTTTCCAGGACCCACTGGAAGCGTGCA	1004
Db	281	LeuGlyPheValSerGluGlnIleArgLysAsnPheAlaTrpThrHisTrpLysArgAla	300
QY	1005	TTCAATGCCACATCATTCCTACGTACATCCGTAAGCTGGGACAAAGCCACAGGGTGAG	1064
Db	301	PheAsnAlaThrLeuPheLeuArgHisIleArgLysLeuGlyGlnIleProGluGlyGlu	320
QY	1065	GAGGCTCCAGGCAGTGTATGACCCGTATAGCCCATAGCCACCCAGGCTTGGGACTAGCCAGTCC	1124
Db	321	GlyAlaSerGluGlnGlyMet**ArgHisSerHis**GlyLeuArgAlaGlyGlnPro	340
QY	1125	CCCAAGTGG 1133	
Db	341	ProLysTrp 343	
RESULT 9			
ID	ABR41269	standard; protein; 270 AA.	
XX	ABR41269;		
AC	ABR41269;		
XX	02-JUN-2003	(first entry)	
DT	02-JUN-2003	(first entry)	
XX	Human DITHP intracellular signalling protein.		
DE	Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;		
XX	cancer; cell proliferative disorder; autoimmune disorder;		
KW	inflammatory disorder; infection; hormonal disorder; metabolic disorder;		
KW	neurological disorder; gastrointestinal disorder; transport disorder;		
KW	connective tissue disorder; drug screening; proteome analysis;		
KW	gene therapy; antisense therapy; genotyping; transgenic animal; knock in;		
KW	disease model; toxicological testing; transcript imaging;		
KW	intracellular signalling.		
XX	Homo sapiens.		
OS	WO200297031-A2.		
PN	05-DEC-2002.		
XX	27-MAR-2002; 2002WO-US010056.		
PF	28-MAR-2001; 2001US-0279619P.		
XX	29-MAR-2001; 2001US-0280067P.		
PR	29-MAR-2001; 2001US-0280068P.		
PR	16-MAY-2001; 2001US-0291280P.		
PR	17-MAY-2001; 2001US-0291829P.		
PR	17-MAY-2001; 2001US-0291849P.		
PR	19-JUN-2001; 2001US-0299428P.		
PR	20-JUN-2001; 2001US-0299776P.		
PR	20-JUN-2001; 2001US-030001P.		
XX	(INCY-) INCYTE GENOMICS INC.		
PA	Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;		
XX	Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;		
PI	Daughter SC, Dam TC, Liu TF, Nguyen DA, Kleeefeld Y, Gerstin EH;		
PI	Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;		
PI	Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;		
XX	WPI; 2003-129518/12.		
DR	N-PSDB; ACC46211.		
XX	Novel human diagnostic and therapeutic polypeptide useful for identifying		
PT	test compound which specifically binds to a polypeptide encoded by human		
PT	diagnostic and therapeutic polynucleotide, and to induce antibodies.		
XX	Claim 27; SEQ ID NO 804; 591pp; English.		
PS	The invention relates to novel human diagnostic and therapeutic		
XX			
CC			

CC polynucleotides designated dithp (ACC46080-ACC46749) and to their encoded  
CC proteins (DITHP; ABR41136-ABR41812). The invention also relates to  
CC polynucleotide sequences at least 90% identical to the dithp cDNA  
CC sequences of the invention; recombinant vectors, host cells and  
CC transgenic organisms comprising a dithp nucleic acid sequence; the  
CC recombinant production of DITHP proteins; antibodies specific for DITHP  
CC proteins; microarrays comprising dithp nucleic acid sequences; methods of  
CC detecting dithp nucleotide and protein sequences; methods of screening  
CC for compounds which specifically bind a DITHP protein; and methods of  
CC assessing the toxicity of test compounds using a dithp hybridisation  
CC probe. Dithp nucleic acid sequences and DITHP proteins may be used in the  
CC diagnosis of a wide variety of conditions including cancer and other cell  
CC proliferative disorders; autoimmune or inflammatory disorders; bacterial,  
CC viral, fungal or parasitic infections; hormonal disorders; metabolic  
CC disorders; neurological disorders; gastrointestinal disorders; transport  
CC disorders; and connective tissue disorders. They may also be used to  
CC screen for modulators of protein activity or gene expression. DITHP  
CC proteins can additionally be used in analysis of the proteome of a tissue  
CC or cell type and to induce antibodies. The dithp nucleic acids are  
CC additionally useful in somatic or germline gene therapy of the disorders  
CC mentioned above, as a source of antisense sequences, as a source of  
CC probes and primers, in genotyping and identification of individuals, in  
CC the generation of transgenic animal models of human disease or knock in  
CC humanised animals, in toxicological testing, and in transcript imaging.  
CC The present sequence represents a DITHP protein which has intracellular  
CC signalling activity. Note: The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 270 AA;

Alignment Scores:  
Pred. No.: 9.65e-96 Length: 270  
Score: 1259.00 Matches: 238  
Percent Similarity: 95.62% Conservative: 2  
Best Local Similarity: 94.82% Mismatches: 11  
Query Match: 43.84% Indels: 0  
DB: 6 Gaps: 0

US-10-032-254A-1 (1-1554) x ABR41269 (1-270)

QY 381 GTAACAGGTGTGAAC TGT TTTGACCGCATCATGGAGCGGGCTCTACACAGAGAAGGAC 440  
Db 20 valThrGlyGlyGluLeuPheAspArgIleMetGluArgGlySerTyrThrGluLysAsp 39  
QY 441 GCCAGCCACTGTAGGGCAGGTCC TTGGCGTGTCTCTCCTACCTCATAGCCTGGGCATC 500  
Db 40 AlaSerHisLeuValGlyGlnValLeuGlyAlaValSerTyrLeuHisSerLeuGlyIle 59  
QY 501 GTGCACCGGACCTCAAGCCTGAAAACCTCCTCTATGCCACACCTTTTGAGGACTCCAAG 560  
Db 60 ValHisArgAspLeuLysProGluAsnLeuLeuTyrAlaThrProPheGluAspSerLys 79  
QY 561 ATCATGGTCTCTGACTTTGGCCTGTCCAAATAACAAGCTGGCAACATGCTAGGCACAGCC 620  
Db 80 IleMetValSerAspPheGlyLeuSerLysIleGlnAlaGlyAsnMetLeuGlyThrAla 99  
QY 621 TGTGGGACCCAGGATATGTGGCCCCAGAGCTCCTGGAGCAGAAACCTACGGGAAGGCC 680  
Db 100 CysGlyThrProGlyTyrValAlaProGluLeuLeuGluGlnLysProTyrGlyLysAla 119  
QY 681 GTAGATGTGTGGCCCTGGGTGTCATCTCTCATCTCTACATCCTGCTGTGTGGGTACCCCCCTTC 740  
Db 120 valAspValTrpAlaLeuGlyValIleSerTyrIleLeuLeuCysGlyTyrProPhe 139  
QY 741 TATGATGAGAGCGATCCTGAACTCTTCAGCAGATTC TGAAGGCCAGCTATGAGTTTGAC 800  
Db 140 TyrAspGluSerAspProGluLeuPheSerGlnIleLeuArgAlaSerTyrGluPheAsp 159  
QY 801 TCCCCCTTTTGGGATGACATCTCAGAATCAGCAAAGACTTTCATTCGCCACCTTCTGGAA 860  
Db 160 SerProPheTrpAspAspIleSerGluSerAlaLysAspPheIleArgHisLeuLeuGlu 179

QY 861 CGTGATCCCCAGAGAGGTTCACTGCCAGCAGCGCCCTACAGCATCTTTGGATCTCTGGG 920  
Db 180 ArgAspProGlnLysArgPheThrCysGlnGlnAlaLeuArgHisLeuTrpIleSerGly 199  
QY 921 GATCAGCCCTTCGATAGGACATCCTGGGTTCTGTCTCAGTGAGCAGATCCAGAAGATTT 980  
Db 200 AspThrAlaPheAspArgAspIleLeuGlySerValSerGluGlnIleArgLysAsnPhe 219  
QY 981 GCCAGGACCCACTGGAAGCGTGCATTCAATGCCACATCATCTCTACGTACATCCGTAAG 1040  
Db 220 AlaArgThrHisTrpLysArgAlaPheAsnAlaThrSerPheLeuArgHisIleArgLys 239  
QY 1041 CTGGGACAAAGCCCGAGGGTGAGGAGGCCCTCCAGGAGTGATGACCCGTCATAGCCAC 1100  
Db 240 LeuGlyGlnIleProGluGlyGluGlyAlaSerGluGlnGlyMetAlaArgHisSerHis 259  
QY 1101 CCAGGCCTTGGGACTAGCCAGTCCCCCAAGTGG 1133  
Db 260 SerGlyLeuArgAlaGlyGlnProProLysTrp 270  
RESULT 10  
ABR41299  
ID ABR41299 standard; protein; 250 AA.  
XX  
AC ABR41299;  
XT  
DT 02-JUN-2003 (first entry)  
XX  
DE Human DITHP intracellular signalling protein.  
XX  
KW Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;  
KW cancer; cell proliferative disorder; autoimmune disorder;  
KW inflammatory disorder; infection; hormonal disorder; metabolic disorder;  
KW neurological disorder; gastrointestinal disorder; transport disorder;  
KW connective tissue disorder; drug screening; proteome analysis;  
KW gene therapy; antisense therapy; genotyping; transgenic animal; knock in;  
KW disease model; toxicological testing; transcript imaging;  
KW intracellular signalling.  
XX  
OS Homo sapiens.  
XX  
PN WO200297031-A2.  
XX  
PD 05-DEC-2002.  
XX  
PF 27-MAR-2002; 2002WO-US010056.  
XX  
PR 28-MAR-2001; 2001US-0279619P.  
PR 29-MAR-2001; 2001US-0280067P.  
PR 29-MAR-2001; 2001US-0280068P.  
PR 16-MAY-2001; 2001US-0291280P.  
PR 17-MAY-2001; 2001US-0291829P.  
PR 17-MAY-2001; 2001US-0291849P.  
PR 19-JUN-2001; 2001US-0299428P.  
PR 20-JUN-2001; 2001US-0299776P.  
PR 20-JUN-2001; 2001US-0300001P.  
XX  
PA (INCY-) INCYTE GENOMICS INC.  
XX  
PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;  
PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;  
PI Daughtery SC, Dam TC, Liu TF, Nguyen DA, Kleeefeld Y, Gerstin EH;  
PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;  
PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;  
XX  
DR WPI; 2003-129518/12.  
DR N-PSDB; ACC46241.  
XX  
PT Novel human diagnostic and therapeutic polypeptide useful for identifying  
PT test compound which specifically binds to a polypeptide encoded by human  
PT diagnostic and therapeutic polynucleotide, and to induce antibodies.  
XX  
PS Claim 27; SEQ ID NO 834; 591pp; English.





CC cells and rapidly moves to the cytoplasm on activation by the kinases  
CC p38/p40/RK. While in the nucleus, MAPKAPK2 contributes to the  
CC phosphorylation of CREB (cAMP response element-binding protein), and is  
CC also responsible for phosphorylating serum response factor and the  
CC transcription factor E47. In the cytoplasm, MAPKAPK2 phosphorylates the  
CC small heat shock protein HSP25/HSP27, lymphocyte specific protein (lusp1),  
CC glycogen synthase, tyrosine hydroxylase (the rate-limiting enzyme in  
CC catecholamine synthesis) and 5-lipoxygenase, a key enzyme in leukotriene  
CC biosynthesis. Mice which lack MAPKAPK2 show increased stree resistance  
CC and survive bacterial LPS-induced endotoxic shock due to a 90% reduction  
CC in the production of TNF-alpha. The crystal structure of MAPKAPK2 may be  
CC used to evaluate the ability of a chemical entity to interact with  
CC binding pockets or other key domains of MAPKAPK2, and in rational drug  
CC design. MAPKAPK2-specific agonists and antagonists identified using the  
CC crystal structure may be used in the treatment of disorders related to  
CC MAPKAPK2. The present sequence represents calcium/calmodulin-dependent  
CC protein kinase I (CamKI), a homologue of MAPKAPK2.

XX  
SQ Sequence 332 AA;

Alignment Scores:

Pred. No.:	1.64e-89	Length:	332
Score:	1184.50	Matches:	220
Percent Similarity:	85.17%	Conservative:	50
Best Local Similarity:	69.40%	Mismatches:	44
Query Match:	41.24%	Indels:	3
DB:	7	Gaps:	2

US-10-032-254A-1 (1-1554) x ADC15044 (1-332)

QY	120	AAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAGCTGGGTCGGGTGCC	179
Db	11	LysGlnAlaGluAspIleArgAspIleTyrAspPheArgAspValLeuGlyThrGlyAla	30
QY	180	TTCTCTGAGTGTGCTGGCCAGGAAGGGGCTCTGCTCATCTTGTGGCCCTCAAGTGC	239
Db	31	PheSerGluValIleLeuAlaGluAspLysArgThrGlnLysLeuValAlaIleLysCys	50
QY	240	ATTCCCCAAGAAAGCACTTCCGGGGCAAGGAGCCCTGGTGGAGAAATGAGATCGCGGTACTT	299
Db	51	IleAlaLysLysAlaLeuGluGlyLysGlySerMetGluAsnGluIleAlaValLeu	70
QY	300	CGCAGAATCAGCCATCCCAACATTGTGGTCTGTGGAGGACGTCCATGAGATCCTTCTCAT	359
Db	71	HisLysIleLysHisProAsnIleValAlaLeuAspAspIleTyrGluSerGlyGlyHis	90
QY	360	CTCTACTTGGCATGGAGCTGGTAACAGTGGTGAACCTGTTTACCGCATCATGGAGCGG	419
Db	91	LeuTyrLeuIleMetGlnLeuValSerGlyGlyGluLeuPheAspArgIleValGluLys	110
QY	420	GGCTCCTACACAGAGAAGGACGCCACCTGTAGGGCAGGTCTCTGGCGTGTCTCC	479
Db	111	GlyPheTyrThrGluArgAspAlaSerArgLeuIlePheGlnValLeuAspAlaValLys	130
QY	480	TACCTTCATAGCTGGGCATCGTGCACCGGACCTCAAGCCTGAAAACCTCCTCTATGCC	539
Db	131	TyrLeuHisAspLeuGlyIleValHisArgAspLeuLysProGluAsnLeuTyrTyr	150
QY	540	ACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTTGGCCTGTCCAAAATACAA---	596
Db	151	SerLeuAspGluAspSerLysIleMetIleSerAspPheGlyLeuSerLysMetGluAsp	170
QY	597	GCTGGCAACATGTAGGCACAGCCTGTGGGACCCAGGATATGTGGCCCCAGAGCTCCTG	656
Db	171	ProGlySerValLeuSerThrAlaCysGlyThrProGlyTyrValAlaProGluValLeu	190
QY	657	GAGCAGAAACCTTACGGGAAGCCGTAGATGTGTGGCCCTGGGTGTCATCTCTACATC	716
Db	191	AlaGlnLysProTyrSerLysAlaValAspCysTrpSerIleGlyValIleAlaTyrIle	210
QY	717	CTGCTGTGTGGGTACCCCCCTTCTATGATGAGAGCGATCCTGAACTCTTCAGCCAGATT	776
Db	211	LeuLeuCysGlyTyrProPheTyrAspGluAsnAspAlaLysLeuPheGluGlnIle	230

QY	777	CTGAGGGCCAGCTATGAGTTTGACTCCCCCTTTTGGGATGACATCTCAGAAATCAGCCAAA	836
Db	231	LeuLysAlaGluTyrGluPheAspSerProTyrTrpAspAspIleSerAspSerAlaLys	250
QY	837	GACTTCATTGCCACCTTCTTGGAAACGTGATCCCCAGAAAGAGGTTTCACCTGCCAGCGCC	896
Db	251	AspPheIleArgHisLeuMetGluLysAspProGluLysArgPheThrCysGluGlnAla	270
QY	897	CTACAGCATCTTTGGATCTCTGGGGATGCAGCCTTCGATAGGGACATCCTGGGTTCTGTC	956
Db	271	LeuGlnHisProTyrIleAlaGlyAspThrAlaLeuAspLysAsnIleHisGlnSerVal	290
QY	957	AGTGAGCAGATCCAGAAAGATTTCGCCAGGACCCACTGGAAGCGTGCATTCAATGCCACA	1016
Db	291	SerGluGlnIleLysLysAsnPheAlaLysSerLysTrpLysGlnAlaPheAsnAlaThr	310
QY	1017	TCATTCTCTACGTACATCCGTAAG-----CTGGGACAAAGCCAGAGGGT	1061
Db	311	AlaValValArgHisMetArgLysLeuGlnLeuGlyHisGlnProGlyGly	327

RESULT 12

AAE34492  
ID AAE34492 standard; protein; 370 AA.

XX AAE34492;

DT 14-MAY-2003 (first entry)

DE Human camKI protein.

XX Human; pyridylpyrimidine derivative; cellular protein kinase; Scrapie;  
KW cellular protein phosphatase; cellular signal transduction; prophylaxis;  
KW prion infection; chronic wasting disease; CWD; Creutzfeldt-Jacob disease;  
KW CJD; transmissible mink encephalopathy; bovine spongiform encephalopathy;  
KW TME; BSE; Gerstmann-Strausler-Scheinker syndrome; GSS; Alpers syndrome;  
KW fatal familial insomnia; FFI; kuru; neurodegenerative disease; nootropic;  
KW Alzheimer's disease; camKI.

XX Homo sapiens.

OS WO200293164-A2.

PD 21-NOV-2002.

PF 16-MAY-2002; 2002WO-EP005420.

XX 16-MAY-2001; 2001EP-00111858.

PR 29-MAY-2001; 2001US-0293528P.

PR 13-JUL-2001; 2001EP-00117113.

PR 18-JUL-2001; 2001US-0305898P.

PA (AXXI-) AXXIMA PHARM AG.

XX Stein-Gerlach M, Salassidis K, Bacher G, Mueller S;

XX WPI; 2003-120714/11.

DR N-PSDB; AAD52784.

XX New pyridylpyrimidine derivatives useful in the treatment or prevention

PT of infectious disease e.g. Kuru syndrome and Creutzfeld-Jacob disease

PT (CJD).

XX Disclosure; Page 77-79; 96pp; English.

XX The invention relates to novel pyridylpyrimidine derivatives and methods  
CC of detecting prion infections and/or prion disease in an individual or in  
CC cells, cell cultures and/or cell lysates. The method involves adding at  
CC least one monoclonal or polyclonal antibody, oligonucleotide or pyridyl-  
CC pyrimidine derivative to the sample or in cells, cell cultures and/or  
CC cell lysates and detecting the activity of at least one human cellular  
CC protein kinases (e.g., FGF-R1 (also known as flg, Fl-1, Flt-2, b-FGFR),  
CC Tkt (also known as CCK-2, DDR-2 or EDDR; EC number 2.7.1.112), Abl (also

known as c-abl), clk1, MKK7 (also known as SAPK1a, SAPKalpha), CDC2 (also known as CDK1), PRK), human cellular protein phosphatases such as PTP-SL (also known as MCP83) and PTP-zeta, the cellular signal transduction molecules HSP80 and GPCR-1. The invention is useful for regulating the production of prions in cells and in the manufacture of pharmaceutical composition for prophylaxis and/or treatment of infectious disease (e.g. Scrapie, chronic wasting disease (CWD), transmissible mink encephalopathy (TME), Creutzfeldt-Jacob disease (CJD), bovine spongiform encephalopathy (BSE), variant CJD, Gerstmann-Straussler-Scheinker syndrome (GSS), fatal familial insomnia (FFI), Kuru and Alpers syndrome, especially BSE, CJD, vCJD) or neurodegenerative diseases (e.g., Alzheimer's disease) in humans or ruminants. The present sequence is human camK1 protein used in the invention

XX  
SQ Sequence 370 AA;

Alignment Scores:	
Pred. No.:	1.7e-89
Score:	1184.50
Percent Similarity:	85.53%
Best Local Similarity:	69.18%
Query Match:	41.24%
DB:	6
Length:	370
Matches:	220
Conservative:	52
Mismatches:	43
Indels:	3
Gaps:	2

US-10-032-254A-1 (1-1554) x AAE34492 (1-370)

QY	120	AAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAAAGCTGGGGCTCGGGTGCC	179
Db	11	LysGlnAlaGluAspIleArgAspIleTyrAspPheArgAspValLeuGlyThrGlyAla	30
QY	180	TTCTCTGAGGTGATCTGGCCAGGAAAGGGCTCTGCTCATCTTGTGGCCCTCAAGTGC	239
Db	31	PheSerGluValIleuAlaGluAspLysArgThrGlnLysLeuValAlaIleLysCys	50
QY	240	ATTCCCAAGAAAGCACTTCGGGGCAAGGAGGCCCTGGTGGAGATGAGATCGCGGTACTT	299
Db	51	IleAlaLysGluAlaLeuGluGlyLysGluGlySerMetGluAsnGluIleAlaValLeu	70
QY	300	CGCAGAATCAGCCATCCCAACATTTGTGGCTCTGGAGGACGTCCATGAGAGTCCTTCTCAT	359
Db	71	HisLysIleLysHisProAsnIleValAlaLeuAspAspIleTyrGluSerGlyGlyHis	90
QY	360	CTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAACCTGTTTGACCGCATCATGGAGCGG	419
Db	91	LeuTyrLeuIleMetGlnLeuValSerGlyGlyGluLeuPheAspArgIleValGluLys	110
QY	420	GGCTCTACACAGAGAAGGACGCCAGCCACCTTGTAGGCGAGGTCCCTGGCGCTGTCTCC	479
Db	111	GlyPheTyrThrGluArgAspAlaSerArgLeuIlePheGlnValLeuAspAlaValLys	130
QY	480	TACCTTCATAGCCTGGGCATCGTGCACCGGACCTCAAGCCCTGAAAACCTCCTCTATGCC	539
Db	131	TyrLeuHisAspLeuGlyIleValHisArgAspLeuLysProGluAsnLeuTyrTyr	150
QY	540	ACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTGGCCTGTCCAAAATACAA---	596
Db	151	SerLeuAspGluAspSerLysIleMetIleSerAspPheGlyLeuSerLysMetGluAsp	170
QY	597	GCTGGCAACATGCTAGGCACAGCCTGTGGACCCAGGATATGTGSCCCAGAGCTCCTG	656
Db	171	ProGlySerValLeuSerThrAlaCysGlyThrProGlyTyrValAlaProGluValLeu	190
QY	657	GAGCAGAAACCTACGGGAAGCCCGTAGATGTGTGGGCCCTGGGTGTCTATCTCCTACATC	716
Db	191	AlaGlnLysProTyrSerLysAlaValAspCysTyrSerIleGlyValIleAlaTyrIle	210
QY	717	CTGCTGTGTGGGTACCCCCCTCTATGATGAGAGCGATCCTGAACCTCTCAGCCAGATT	776
Db	211	LeuLeuCysGlyTyrProProPheTyrAspGluAsnAspAlaLysLeuPheGluGlnIle	230
QY	777	CTGAGGGCCAGCTATGAGTTTGACTCCCCCTTTTGGGATGACATCTCAGAATCAGCCAAA	836
Db	231	LeuLysAlaGluTyrGluPheAspSerProTyrTyrAspAspIleSerAspSerAlaLys	250



Db 11 LysGlnAlaGluAspIleArgAspIleTyrAspPheArgAspValLeuGlyThrGlyAla 30  
QY 180 TTCTCTGAGGTGATGCTGGCCAGGAAAGGGCTCTGCTCATCTTGTGGCCCTCAAGTGC 239  
Db 31 PheSerGluValIleLeuAlaGluAspLysArgThrGlnLysLeuValAlaIleLysCys 50  
QY 240 ATTCCTCAAGAACACTTCGGGGCAAGGAGCCCTGGTGGAGAAATGAGATCGCGGTACTT 299  
Db 51 IleAlaLysGluAlaLeuGluGlyLysGlySerMetGluAsnGluIleAlaValLeu 70  
QY 300 CGCAGAAATCAGCCATCCCAACATTGTGGCTCTGGAGGACGTCCATGAGAGTCCTTCTCAT 359  
Db 71 HisLysIleLysHisProAsnIleValAlaLeuAspAspIleTyrGluSerGlyGlyHis 90  
QY 360 CTCTACTTGGCCATGAGCTGGTAAACAGGTGGTAACTGTTTACC GCATCATGGAGCGG 419  
Db 91 LeuTyrLeuIleMetGlnLeuValSerGlyGlyGluLeuPheAspArgIleValGluLys 110  
QY 420 GGCTCTACACAGAGAAGGACGCCAGCCACCTTGTAGGGCAGGTCTTGGCGTGTCTCC 479  
Db 111 GlyPheTyrThrGluArgAspAlaSerArgLeuIlePheGlnValLeuAspAlaValLys 130  
QY 480 TACCTTCATAGCTGGGCATCGTGCCACGGGACCTCAAGCCTGAAACCTCCTCTATGCC 539  
Db 131 TyrLeuHisAspLeuGlyIleValHisArgAspLeuLysProGluAsnLeuTyrTyr 150  
QY 540 ACACCTTTGAGGACTCCAAGATCATGTTCTGTGACTTTGGCCCTGTCCAAATACAA --- 596  
Db 151 SerLeuAspGluAspSerLysIleMetIleSerAspPheGlyLeuSerLysMetGluAsp 170  
QY 597 GCTGGCAACATGCTAGGCACAGCCTGTGGACCCAGGATATGTGGCCCGAGACTCCTG 656  
Db 171 ProGlySerValLeuSerThrAlaCysGlyThrProGlyTyrValAlaProGluValLeu 190  
QY 657 GAGCAGAAACCTTACGGGAAGCCGTAGATGTGTGGCCCTGGGTGTCATCTCTACATC 716  
Db 191 AlaGlnLysProTyrSerLysAlaValAspCysTrpSerIleGlyValIleAlaTyrIle 210  
QY 717 CTGCTGTGTGGGTACCCCTTCTATGATGAGAGCGATCCTGAACTTTCAGCCAGATT 776  
Db 211 LeuLeuCysGlyTyrProPheTyrAspGluAsnAspAlaLysLeuPheGluGlnIle 230  
QY 777 CTGAGGGCCAGCTATGAGTTTGACTCCCTTTTGGGATGACATCTCAGAATCAGCCAAA 836  
Db 231 LeuLysAlaGluTyrGluPheAspSerProTyrTrpAspAspIleSerAspSerAlaLys 250  
QY 837 GACTTCATTGCGCACCTTCTGGAACGTGATCCCGAGGACCGAGGTTTCACTGCCAGCGCC 896  
Db 251 AspPheIleArgHisLeuMetGluLysAspProGluLysArgPheThrCysGluGlnAla 270  
QY 897 CTACAGCATCTTTGGATCTCTGGGGATGCAGCCTTCGATAGGGACATCCTGGGTTCTGTC 956  
Db 271 LeuGlnHisProTrpIleAlaGlyAspThrAlaLeuAspLysAsnIleHisGlnSerVal 290  
QY 957 AGTGAGCAGATCCAGAGAATAATTTGCCAGGACCCACTGGAAGCGTGCATTCAATGCCACA 1016  
Db 291 SerGluGlnIleLysLysAsnPheAlaLysSerLysTrpLysGlnAlaPheAsnAlaThr 310  
QY 1017 TCATTCTCAGTCACATCCCTAAG-----CTGGACAAAGCCAGAGGTTGAG 1064  
Db 311 AlaValValArgHisMetArgLysLeuGlnLeuGlyThrSerGlnGluGlyGln 328  
RESULT 14  
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XX  
AC ADL97820;  
XX  
DT 03-JUN-2004 (first entry)  
XX  
DE Human CAMKI protein SeqID 6.  
XX

KW human; neuropsychiatric disorder; bipolar disorder; schizophrenia;  
KW alpha-type II calcium/calmodulin dependent protein kinase; CAMKII-alpha;  
KW TBR1; Brachyury; neuroleptic; antidepressant; gene therapy;  
KW mental disorder; mood disorder; psychosis; major depression; CAMKI.  
OS Homo sapiens.  
XX  
PN WO2004020455-A2.  
XX  
PD 11-MAR-2004.  
XX  
PF 26-AUG-2003; 2003WO-US026873.  
XX  
PR 28-AUG-2002; 2002US-0406879P.  
PR 27-FEB-2003; 2003US-0451306P.  
XX  
PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
XX  
PI Bunney WR, Jones EG, Molnar M;  
XX  
DR WPI; 2004-239152/22.  
DR N-PSDB; ADL97819.  
XX  
PT Determining whether a subject has or is predisposed to a mental disorder,  
PT comprises detecting the level of reagent that selectively associates with  
PT a specified polynucleotide or polypeptide in a sample from the subject.  
XX  
PS Disclosure; SEQ ID NO 6; 85pp; English.  
XX  
CC This invention relates to a novel method to determine whether a subject  
CC has or is predisposed to a mental or neuropsychiatric disorder.  
CC Specifically, it refers to identifying modulators of two genes expressed  
CC in the central nervous system of patients suffering from bipolar disorder  
CC or schizophrenia, namely alpha-type II calcium/calmodulin dependent  
CC protein kinase (CAMKII-alpha) and TBR1 (a putative transcription factor  
CC related to the Brachyury gene). The present invention describes screening  
CC assays used to identify gene expression modulators, as well as  
CC appropriate antibodies, agonists and antagonists thereof. Accordingly,  
CC these compositions, which exhibit neuroleptic and antidepressant  
CC activities can also be used for gene therapy purposes to treat the  
CC aforementioned conditions, and mental disorders including mood disorders,  
CC psychosis and major depression. This polypeptide sequence is the human  
CC CAMKI protein of the invention.  
XX  
SQ Sequence 370 AA;  
Alignment Scores:  
Pred. No.: 1.7e-89 Length: 370  
Score: 1184.50 Matches: 220  
Percent Similarity: 85.53% Conservative: 52  
Best Local Similarity: 69.18% Mismatches: 43  
Query Match: 41.24% Indels: 3  
DB: 8 Gaps: 2  
US-10-032-254A-1 (1-1554) x ADL97820 (1-370)  
QY 120 AAACAGACGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAGCTGGGTCGGGTGCC 179  
Db 11 LysGlnAlaGluAspIleArgAspIleTyrAspPheArgAspValLeuGlyThrGlyAla 30  
QY 180 TTCTCTGAGGTGATGCTGGCCAGGAAAGGGCTCTGCTCATCTTGTGGCCCTCAAGTGC 239  
Db 31 PheSerGluValIleLeuAlaGluAspLysArgThrGlnLysLeuValAlaIleLysCys 50  
QY 240 ATTCCTCAAGAACACTTCGGGGCAAGGAGCCCTGGTGGAGAAATGAGATCGCGGTACTT 299  
Db 51 IleAlaLysGluAlaLeuGluGlyLysGlySerMetGluAsnGluIleAlaValLeu 70  
QY 300 CGCAGAAATCAGCCATCCCAACATTGTGGCTCTGGAGGACGTCCATGAGAGTCCTTCTCAT 359  
Db 71 HisLysIleLysHisProAsnIleValAlaLeuAspAspIleTyrGluSerGlyGlyHis 90  
QY 360 CTCTACTTGGCCATGAGCTGGTAAACAGGTGGTAACTGTTTGGAGCGG 419

Db 91 LeuTyrLeuIleMetGlnLeuValSerGlyGlyGluLeuPheAspArgIleValGluLys 110  
QY 420 GGCTCCTACACAGAGAAGGACGCCAGCCACTGTGTAGGGCAGGTCCTTGGCGCTGTCTCC 479  
Db 111 GlyPheTyrThrGluArgAspAlaSerArgLeuIlePheGlnValLeuAspAlaValLys 130  
QY 480 TACCTTCATAGCTGGGCATCGTGCACCGGACCTCAAGCCTGAACCTCCTCTATGCC 539  
Db 131 TyrLeuHisAspLeuGlyIleValHisArgAspLeuLysProGluAsnLeuLeuTyrTyr 150  
QY 540 ACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTGGCCTGTCCAAAATACAA--- 596  
Db 151 SerLeuAspGluAspSerLysIleMetIleSerAspPheGlyLeuSerLysMetGluAsp 170  
QY 597 GCTGGCAACATCGTAGGCACAGCCTGTGGACCCAGGATATGTGGCCCGCAGAGCTCCTG 656  
Db 171 ProGlySerValLeuSerThrAlaCysGlyThrProGlyTyrValAlaProGluValLeu 190  
QY 657 GAGCAGAAACCTACGGGAAGCCGTAGATGTGTGGCCCTGGGTGTCATCTCTACATC 716  
Db 191 AlaGlnLysProTyrSerLysAlaValAspCysTrpSerIleGlyValIleAlaTyrIle 210  
QY 717 CTGCTGTGTGGTACCCCTCTTCTATGATGAGAGCGATCCTGAACTCTTCAGCCAGATT 776  
Db 211 LeuLeuCysGlyTyrProPheTyrAspGluAsnAspAlaLysLeuPheGluGlnIle 230  
QY 777 CTGAGGGCCAGCTATGAGTTTGACTCCCTCTTTGGGATGACATCTCAGAATCAGCCAAA 836  
Db 231 LeuLysAlaGluTyrGluPheAspSerProTyrTrpAspAspIleSerAspSerAlaLys 250  
QY 837 GACTTCATTGCCACCTTCTGGAAACGTGATCCCCAGAGAGGTTCACTGCCAGAGGCC 896  
Db 251 AspPheIleArgHisLeuMetGluLysAspProGluLysArgPheThrCysGluGlnAla 270  
QY 897 CTACAGCATCTTTGGATCTCTGGGATGCAGCCTTCGATAGGGACATCTGGGTTCTGTC 956  
Db 271 LeuGlnHisProTrpIleAlaGlyAspThrAlaLeuAspLysAsnIleHisGlnSerVal 290  
QY 957 AGTGAGCAGATCCAGAAGAATTTGCCAGGACCCACTGGAAGCGTGCAATTCAATGCCACA 1016  
Db 291 SerGluGlnIleLysLysAsnPheAlaLysSerLysTrpLysGlnAlaPheAsnAlaThr 310  
QY 1017 TCATTCTCTACATCCGTAAG-----CTGGGACAAAGCCAGAGGGTGAG 1064  
Db 311 AlaValValArgHisMetArgLysLeuGlnLeuGlyThrSerGlnGluGlyGln 328  
RESULT 15  
ADP23704  
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XX  
AC ADP23704;  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE PRO polypeptide SEQ ID NO:882.  
XX  
KW PRO; antiinflammatory; antiarthritic; antirheumatic; immunosuppressive;  
KW osteopathic; antidiabetic; dermatological; antipsoriatic; antiallergic;  
KW antiasthmatic; hepatotropic; respiratory; gene therapy; immune system.  
XX  
OS Unidentified.  
XX  
PN WO2004041170-A2.  
XX  
PD 21-MAY-2004.  
XX  
PF 30-OCT-2003; 2003WO-US034312.  
XX  
PR 01-NOV-2002; 2002US-0423394P.  
XX  
PA (GETH ) GENENTECH INC.  
XX

PI Clark H, Schoenfeld J, Van Lookeren M, Williams PM, Wood WI;  
PI Wu TD;  
XX  
DR WPI; 2004-419628/39.  
DR N-PSDB; ADP23703.  
XX  
PT New PRO polypeptides and polynucleotides, useful for treating e.g.  
PT erythematosis, rheumatoid arthritis, diabetes mellitus, immune-mediated  
PT renal disease, or demyelinating diseases of the central or peripheral  
PT nervous system.  
XX  
PS Claim 7; SEQ ID NO 882; 2940pp; English.  
XX  
CC The invention relates to a novel isolated nucleic acid and the PRO  
CC polypeptide encoded by it. A protein of the invention has  
CC antiinflammatory, antiarthritic, antirheumatic, immunosuppressive,  
CC osteopathic, antidiabetic, dermatological, antipsoriatic, antiallergic,  
CC antiasthmatic, hepatotropic, and respiratory activity. A polynucleotide  
CC of the invention may have a use in gene therapy. The PRO polypeptide, its  
CC agonist, antagonist, or antibody that specifically binds to the  
CC polypeptide is useful for treating an immune related disorder such as  
CC systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis,  
CC juvenile chronic arthritis, a spondyloarthropathy, systemic sclerosis, an  
CC idiopathic inflammatory myopathy, Sjogren's syndrome, autoimmune  
CC vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune  
CC thrombocytopenia, thyroiditis, diabetes mellitus, immune-mediated renal  
CC disease, a demyelinating disease of the central or peripheral nervous  
CC system, idiopathic demyelinating polyneuropathy, Guillain-Barre syndrome,  
CC a chronic inflammatory demyelinating polyneuropathy, a hepatobiliary  
CC disease, infectious or autoimmune chronic active hepatitis, primary  
CC biliary cirrhosis, granulomatous hepatitis, sclerosing cholangitis,  
CC inflammatory bowel disease, gluten-sensitive enteropathy, Whipple's  
CC disease, an autoimmune or immune-mediated skin disease, a bullous skin  
CC disease, erythema multiforme, contact dermatitis, psoriasis, an allergic  
CC disease, asthma, allergic rhinitis, atopic dermatitis, food  
CC hypersensitivity, urticaria, an immunologic disease of the lung,  
CC eosinophilic pneumonia, idiopathic pulmonary fibrosis, hypersensitivity  
CC pneumonitis, a transplantation associated disease, graft rejection or  
CC graft-versus-host disease. The present sequence represents a PRO protein  
CC of the invention.  
XX  
SQ Sequence 370 AA;  
Alignment Scores:  
Pred. No.: 1.7e-89 Length: 370  
Score: 1184.50 Matches: 220  
Percent Similarity: 85.53% Conservative: 52  
Best local Similarity: 69.18% Mismatches: 43  
Query Match: 41.24% Indels: 3  
DB: 8 Gaps: 2  
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Db 11 LysGlnAlaGluAspIleArgAspIleTyrAspPheArgAspValLeuGlyThrGlyAla 30  
QY 180 TTCTCTGAGGTGATGCTGGCCCGGAGGAGGGGCTCTGCTCATCTTGTGGCCCTCAAGTGC 239  
Db 31 PheSerGluValIleLeuAlaGluAspLysArgThrGlnLysLeuValAlaIleLysCys 50  
QY 240 ATCCCAAGAAAGCACCTTCGGGGCAAGGAGGCCCTGGTGAGAGATGAGATCGCGGTACTT 299  
Db 51 IleAlaLysGluAlaLeuGluGlyLysGluGlySerMetGluAsnGluIleAlaValLeu 70  
QY 300 CGCAGAAATCAGCCATCCCAACATTGTGGTCTCTGGAGGACGTCCATGAGAGTCTTCTCAT 359  
Db 71 HisLysIleLysHisProAsnIleValAlaLeuAspAspIleTyrGluSerGlyGlyHis 90  
QY 360 CTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAAGTCTTTGACCGCATCATGGAGCGG 419  
Db 91 LeuTyrLeuIleMetGlnLeuValSerGlyGlyGluLeuPheAspArgIleValGluLys 110





GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model  
Run on: June 6, 2005, 09:50:10 ; Search time 45 Seconds  
(without alignments)  
5155.762 Million cell updates/sec

Title: US-10-032-254A-1  
Perfect score: 2872  
Sequence: 1 gttgcgagtcctccactc.....caaaaaaaaaaaaaaa 1554

Scoring table: BLOSUM62  
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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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- 3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*
- 4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep:\*
- 5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
- 6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1808	63.0	358	4	US-09-230-896C-29 Sequence 29, Appl
2	1625	56.6	343	2	US-08-878-989-5 Sequence 5, Appli
3	1625	56.6	343	3	US-09-272-796-5 Sequence 5, Appli
4	1190	41.4	415	4	US-09-949-016-7461 Sequence 7461, Ap
5	1190	41.4	415	4	US-09-949-016-7462 Sequence 7462, Ap
6	1184.5	41.2	370	2	US-08-878-989-19 Sequence 19, Appl
7	1184.5	41.2	370	3	US-09-272-796-19 Sequence 19, Appl
8	1184.5	41.2	370	3	US-09-457-040B-31 Sequence 31, Appl
9	1184.5	41.2	370	4	US-09-538-092-1314 Sequence 1314, Ap
10	1173.5	40.9	385	4	US-09-733-388-2 Sequence 2, Appli
11	1173.5	40.9	385	4	US-10-446-175-2 Sequence 2, Appli
12	1169.5	40.7	355	4	US-09-579-664B-10 Sequence 10, Appl

13	1169.5	40.7	355	4	US-10-355-975A-10	Sequence 10, Appl
14	1157	40.3	356	4	US-09-733-388-4	Sequence 4, Appli
15	1157	40.3	356	4	US-10-446-175-4	Sequence 4, Appli
16	1065	37.1	476	4	US-09-960-643-2	Sequence 2, Appli
17	730	25.4	473	4	US-09-538-092-1353	Sequence 1353, Ap
18	725	25.2	501	4	US-09-734-030-2	Sequence 2, Appli
19	725	25.2	501	4	US-10-153-921-2	Sequence 2, Appli
20	725	25.2	501	4	US-09-797-039-2	Sequence 2, Appli
21	725	25.2	501	4	US-10-669-689-2	Sequence 2, Appli
22	669	23.3	424	2	US-08-715-568A-1	Sequence 1, Appli
23	659	22.9	729	4	US-09-949-016-6544	Sequence 6544, Ap
24	659	22.9	794	4	US-09-949-016-9883	Sequence 9883, Ap
25	639.5	22.3	264	2	US-07-857-224B-24	Sequence 24, Appl
26	637	22.2	766	4	US-09-975-326-2	Sequence 2, Appli
27	637	22.2	766	4	US-10-217-357-2	Sequence 2, Appli
28	634.5	22.1	765	4	US-09-975-326-4	Sequence 4, Appli
29	634.5	22.1	765	4	US-10-217-357-4	Sequence 4, Appli
30	594.5	20.7	264	2	US-07-857-224B-18	Sequence 18, Appl
31	591	20.6	463	1	US-07-951-715A-25	Sequence 25, Appl
32	591	20.6	463	2	US-08-459-448A-25	Sequence 25, Appl
33	591	20.6	463	3	US-08-459-595A-25	Sequence 25, Appl
34	591	20.6	463	3	US-08-459-504B-25	Sequence 25, Appl
35	591	20.6	463	3	US-08-459-444-25	Sequence 0, Appli
36	591	20.6	463	3	US-09-547-422-25	Sequence 0, Appli
37	591	20.6	463	4	US-09-988-462-25	Sequence 25, Appl
38	589.5	20.5	817	4	US-09-992-481-4	Sequence 4, Appli
39	589.5	20.5	817	4	US-10-434-034-4	Sequence 4, Appli
40	589	20.5	565	3	US-09-800-960-2	Sequence 2, Appli
41	589	20.5	565	4	US-10-096-960-2	Sequence 2, Appli
42	584.5	20.4	639	3	US-09-347-801-17	Sequence 17, Appl
43	584.5	20.4	639	4	US-09-854-731-17	Sequence 17, Appl
44	584	20.3	556	3	US-09-800-960-4	Sequence 4, Appli
45	584	20.3	556	4	US-10-096-960-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-09-230-896C-29  
; Sequence 29, Application US/092330896C  
; Patent No. 6635479  
; GENERAL INFORMATION:  
; APPLICANT: The Scripps Research Institute  
; APPLICANT: Sutcliffe, et al.  
; TITLE OF INVENTION: Hypothalamus-Specific Polypeptides  
; FILE REFERENCE: TSRI-548.1  
; CURRENT APPLICATION NUMBER: US/09/230,896C  
; CURRENT FILING DATE: 1999-02-02  
; PRIOR APPLICATION NUMBER: 60/023,220  
; PRIOR FILING DATE: 1996-08-02  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 29  
; LENGTH: 358  
; TYPE: PRT  
; ORGANISM: ratus ratus  
US-09-230-896C-29

Alignment Scores:  
Pred. No.: 5.55e-158 Length: 358  
Score: 1808.00 Matches: 353  
Percent Similarity: 98.60% Conservative: 0  
Best Local Similarity: 98.60% Mismatches: 5  
Query Match: 62.95% Indels: 1  
DB: 4 Gaps: 0

US-10-032-254A-1 (1-1554) x US-09-230-896C-29 (1-358)

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QY 165 CTGGGCTCGGGTGCCTTCTCTGAGGTGATGCTGGCCAGGAAAGGGGCTCTGCTCATCTT 224

Db 21 LeuGlySerGlyAlaPheSerGluValMetLeuAlaGlnGluArgGlySerAlaHisLeu 40  
QY 225 GTGGCCCTCAAGTGCATTCCCAAGAAAGCACTTCGGGGCAAGGAGGCCTGGTGGAGAAT 284  
Db 41 ValAlaLeuLysCysIleProLysLysAlaLeuArgGlyLysGluAlaLeuValGluAsn 60  
QY 285 GAGATCGCGGTACTTCGCAGAATCAGCCATCCCAACATTGTGGCTCTGGAGGACGTCCAT 344  
Db 61 GluIleAlaValLeuArgArgIleSerHisProAsnIleValAlaLeuGluAspValHis 80  
QY 345 GAGATCCCTTCTCATCTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAACGTGTTGAC 404  
Db 81 GluSerProSerHisLeuTyrLeuAlaMetGluLeuValThrGlyGlyGluLeuPheAsp 100  
QY 405 CGCATCATGGAGGGGGCTCCTACACAGAGAAGACGCCAGCCACCTGTAGGGCAGGTC 464  
Db 101 ArgIleMetGluArgGlySerTyrThrGluLysAspAlaSerHisLeuValGlyGlnVal 120  
QY 465 CTTGGCGCTGTCTCCTACCTTTCATAGCCTGGGATCGTGCACCGGAGCTCAAGCCTGAA 524  
Db 121 LeuGlyAlaValSerTyrLeuHisSerLeuGlyIleValHisArgAspLeuLysProGlu 140  
QY 525 AACCTCCTCTATGCACACACCTTTTGAGGACTCCAAAGATCATGGTCTCTGACTTTGGCCTG 584  
Db 141 AsnLeuLeuTyrAlaThrProPheGluAspSerLysIleMetValSerAspPheGlyLeu 160  
QY 585 TCCAAAATACAAGCTGGCAACATGCTAGGCACAGCCTGTGGGACCCAGGATATGTGGCC 644  
Db 161 SerLysIleGlnAlaGlyAsnMetLeuGlyThrAlaCysGlyThrProGlyTyrValAla 180  
QY 645 CCAGAGCTCCTGGAGCAGAAACCTTACGGGAAGGCCGTAGATGTGTGGCCCTGGGTGC 704  
Db 181 ProGluLeuLeuGluGlnLysProTyrGlyLysAlaValAspValTrpAlaLeuGlyVal 200  
QY 705 ATCTCCTACATCCTGCTGTGTGGGTACCCCTTCTATGATGAGAGGATCCTGAACTC 764  
Db 201 IleSerTyrIleLeuLeuCysGlyTyrProProPheTyrAspGluSerAspProGluLeu 220  
QY 765 TTCAGCCAGATTCTGAGGGCCAGCTATGAGTTTGACTCCCTCTTTGGGATGACATCTCA 824  
Db 221 PheSerGlnIleLeuArgAlaSerTyrGluPheAspSerProPheTrpAspAspIleSer 240  
QY 825 GAATCAGCCCAAAGACTTCATTTCGCCACCTTCTGGAACGTGATCCCCAGAGAGGTTTACC 884  
Db 241 GluSerAlaLysAspPheIleArgHisLeuLeuGluArgAspProGlnLysArgPheThr 260  
QY 885 TGCCAGCAGGCCCTACAGCATCTTTGGATCTCTGGGGATGCAGCCTTCGATAGGGACATC 944  
Db 261 CysGlnGlnAlaLeuGlnHisLeuTrpIleSerGlyAspAlaAlaLeuAspArgAspIle 280  
QY 945 CTGGGTTCTGTCAGTGAGCAGATCCAGAAGATTTTGCAGGACCCACTGGAAGCGTGCA 1004  
Db 281 LeuGlySerValSerGluGlnIleGlnLysAsnPheAlaArgThrHisTrpLysArgAla 300  
QY 1005 TTCAATGCCACATCATTCCTACGTACATCCGTAAGCTGGGACAAAGCCAGAGGGTGAG 1064  
Db 301 PheAsnAlaThrSerPheLeuArgHisIleArgLysLeuGlyGlnSerProGluGlyGlu 320  
QY 1065 GAGGCCCTCCAGGCAGTGTATGACCCGTCATAGCCACCCAGGCCCTTGGGACTAGCCAGTCC 1124  
Db 321 GluAlaSerArgGlnGlyMetThrArgHisSerHisProGlyLeuGlyThrSerGlnSer 340  
QY 1125 CCCAAGTGGTG-AAAACCAGGTAGATGCCAAGGAGCCCAAGTGGACTGACTCC 1177  
Db 341 ProLysTrpValThrThrArgTrpMetProArgLysAlaLysTrpThrAspSer 358

RESULT 2  
US-08-878-989-5  
; Sequence 5, Application US/08878989  
; Patent No. 5885803  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga

; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guegler, Karl G.  
; APPLICANT: Lal, Preeti  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Shah, Purvi  
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN  
; TITLE OF INVENTION: KINASES  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/878,989  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J J  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0321 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 343 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: PROSNOT06  
; CLONE: 827431  
; US-08-878-989-5

Alignment Scores:  
Pred. No.: 4.05e-141 Length: 343  
Score: 1625.00 Matches: 316  
Percent Similarity: 93.29% Conservative: 4  
Best local Similarity: 92.13% Mismatches: 23  
Query Match: 56.58% Indels: 0  
DB: 2 Gaps: 0

US-10-032-254A-1 (1-1554) x US-08-878-989-5 (1-343)

QY 105 ATGCTGCTGCTCAAGAAACAGACGAGGACATCAGCAGTGTCTATGATCCGGGAGAAG 164  
Db 1 MetLeuLeuLysLysHisThrGluAspIleSerSerValTyrGluIleArgGluArg 20  
QY 165 CTGGGCTCGGTCCTTCTCTGAGGTGATCTGGCCCAGGAAAGGGCTCTGCTCATCTT 224  
Db 21 LeuGlySerGlyAlaPheSerGluValValLeuAlaGlnGluArgGlySerAlaHisLeu 40  
QY 225 GTGGCCCTCAAGTGCATTTCCCAAGAAAGCACTTCGGGGCAAGGAGGCCCTGGTGGAGAAT 284  
Db 41 ValAlaLeuLysCysIleProLysLysAlaLeuArgGlyLysGluAlaLeuValGluAsn 60  
QY 285 GAGATCGCGGTACTTCGCAGAATCAGCCATCCCAACATTGTGGCTCTGAGGACGTCCAT 344  
Db 61 GluIleAlaValLeuArgArgIleSerHisProAsnIleValAlaLeuGluAspValHis 80

QY 345 GAGAGTCCTTCTCATCTCTACTTTGGCCATGGAGCTGGTAACAGGTGGTGAACCTGTTTGAC 404  
Db 81 GluSerProSerHisLeuTyrLeuAlaMetGluLeuValThrGlyGlyGluLeuPheAsp 100  
QY 405 CGCATCATGAGCGGGGCTCCTACACAGAGAAGGACGCCAGCCACTTGTTAGGCGAGTC 464  
Db 101 ArgIleMetGluArgGlySerTyrThrGluLysAspAlaSerHisLeuValGlyGlnVal 120  
QY 465 CTTGGCGTGTCTCTCTACCTTCATAGCTGGGCATCGTGCAACCGGACCTCAAGCCTGAA 524  
Db 121 LeuGlyAlaValSerTyrLeuHisSerLeuGlyIleValHisArgAspLeuLysProGlu 140  
QY 525 AACCTCCTCATGCCACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTGGCCTG 584  
Db 141 AsnLeuLeuTyrAlaThrProPheGluAspSerLysIleMetValSerAspPheGlyLeu 160  
QY 585 TCCAAAATACAAAGCTGGCAACATGCTAGGCACAGCCTGTGGACCCAGGATATGTGGCC 644  
Db 161 SerLysIleGlnAlaGlyAsnMetLeuGlyThrAlaCysGlyThrProGlyTyrValAla 180  
QY 645 CCAGAGCTCTTGAGCAGAAACCTACGGGAAGCCGTAGATGTGTGGCCCTGGGTGTC 704  
Db 181 ProGluLeuLeuGluGlnLysProTyrGlyLysAlaValAspValTrpAlaLeuGlyVal 200  
QY 705 ATCTCCTACATCTGTGTGTGGGTACCCCTCTCTATGATGAGAGCGATCCTGAATC 764  
Db 201 IleSerTyrIleLeuLeuCysGlyTyrProProPheTyrAspGluSerAspProGluLeu 220  
QY 765 TTCAGCCAGATTCTGAGGGCCAGCTATGAGTTTGACTCCCTCTTTGGGATGACATCTCA 824  
Db 221 PheSerGlnIleLeuArgAlaSerTyrGluPheAsp\*\*ProPheTrpAspAspIleSer 240  
QY 825 GAATCAGCCAAAAGACTTCATTTCGCCACCTTCTTGAAACGTGATCCCCAGAGAGTTTCACC 884  
Db 241 GluSerGlyLysAspPheIleArgHisLeuLeuGluArgAspLeuGlnLysArgPheThr 260  
QY 885 TGCCAGCAGCCCTACAGCATCTTTGGATCTCTGGGGATGCAGCCCTTCGATAGGGACATC 944  
Db 261 CysGlnGlnAlaLeuArgAspLeuTrpIlePheTrpAspThrGlyPheGlyArgAspIle 280  
QY 945 CTGGGTTCTGTCTAGTGAGCAGATCCAGAGAATTTTGCCAGGACCCACTGGAAGCGTGCA 1004  
Db 281 LeuGlyPheValSerGluGlnIleArgLysAsnPheAlaTrpThrHisTrpLysArgAla 300  
QY 1005 TTCAATGCCACATCATCTCTACGTCACTCCGTAAGCTGGGACAAAGCCAGAGGTGAG 1064  
Db 301 PheAsnAlaThrLeuPheLeuArgHisIleArgLysLeuGlyGlnIleProGluGlyGlu 320  
QY 1065 GAGGCTCCAGGCAGTGATGACCCCGTCATAGCCACCCAGGCCCTTGGGACTAGCCAGTCC 1124  
Db 321 GlyAlaSerGluGlnGlyMet\*\*ArgHisSerHis\*\*GlyLeuArgAlaGlyGlnPro 340  
QY 1125 CCCAAGTGG 1133  
Db 341 ProLysTrp 343

RESULT 3

US-09-272-796-5  
; Sequence 5, Application US/09272796  
; Patent No. 6207148

GENERAL INFORMATION:

; APPLICANT: Bandman, Olga  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guegler, Karl G.  
; APPLICANT: Lal, Preeti  
; APPLICANT: Goli, Surya K.  
; APPLICANT: Shah, Purvi  
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN  
; TITLE OF INVENTION: KINASES  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/272,796  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/878,989  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J J  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0321 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 343 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: PROSNOT06  
; CLONE: 827431  
; US-09-272-796-5

Alignment Scores:

Pred. No.: 4.05e-141 Length: 343  
Score: 1625.00 Matches: 316  
Percent Similarity: 93.29% Conservative: 4  
Best local Similarity: 92.13% Mismatches: 23  
Query Match: 56.58% Indels: 0  
DB: 3 Gaps: 0

US-10-032-254A-1 (1-1554) x US-09-272-796-5 (1-343)

QY 105 ATGCTGCTGCTCAAGAAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAAG 164  
Db 1 MetLeuLeuLeuLysHisThrGluAspIleSerSerValTyrGluIleArgGluArg 20  
QY 165 CTGGGCTCGGTGCCTTCTCTGAGGTGATCTGCCCCAGGAAAGGGCTCTGCTCATCTT 224  
Db 21 LeuGlySerGlyAlaPheSerGluValValLeuAlaGlnGluArgGlySerAlaHisLeu 40  
QY 225 GTGGCCCTCAAGTGCATTCCCAAGAAAGCACTTCGGGGCAAGGAGGCCCTGGTGAGAAAT 284  
Db 41 ValAlaLeuLysCysIleProLysLysAlaLeuArgGlyLysGluAlaLeuValGluAsn 60  
QY 285 GAGATCGGTACTTCGCAGAATCAGCCATCCCAACATTGTGGCTCTGGAGGACGTCCAT 344  
Db 61 GluIleAlaValLeuArgArgIleSerHisProAsnIleValAlaLeuGluAspValHis 80  
QY 345 GAGAGTCCTTCTCATCTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAACCTGTTTGAC 404  
Db 81 GluSerProSerHisLeuTyrLeuAlaMetGluLeuValThrGlyGlyLeuPheAsp 100  
QY 405 CGCATCATGAGCGGGGCTCCTACACAGAGAAGGACGCCAGCCACTTGTTAGGCGAGTC 464  
Db 101 ArgIleMetGluArgGlySerTyrThrGluLysAspAlaSerHisLeuValGlyGlnVal 120  
QY 465 CTTGGCGTGTCTCTCTACCTTCATAGCTGGGCATCGTGCAACCGGACCTCAAGCCTGAA 524  
Db 121 LeuGlyAlaValSerTyrLeuHisSerLeuGlyIleValHisArgAspLeuLysProGlu 140





Db 336 SerGluGlnIleLysLysAsnPheAlaLysSerLysTrpLysGlnAlaPheAsnAlaThr 355

QY 1017 TCATTCCTACGTCACATCCGTAAG-----CTGGGACAAAGCCCGAGGGTGAG 1064

Db 356 AlaValValArgHisMetArgLysLeuGlnLeuGlyThrSerGlnGluGlyGln 373

RESULT 5

US-09-949-016-7462

; Sequence 7462, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; PRIOR FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 7462

; LENGTH: 415

; TYPE: PRT

; ORGANISM: Human

US-09-949-016-7462

Alignment Scores:

Pred. No.:	5.68e-101	Length:	415
Score:	1190.00	Matches:	227
Percent Similarity:	78.49%	Conservative:	54
Best Local Similarity:	63.41%	Mismatches:	53
Query Match:	41.43%	Indels:	24
DB:	4	Gaps:	4

US-10-032-254A-1 (1-1554) x US-09-949-016-7462 (1-415)

QY 15 CCACTCCGAGGCGCCAGGGCCCAAGCAGCGATTAGGTGG-----CTGCGT 59

Db 32 ProArgArgGlyAlaLeuAlaValValGlyGlyGlnTrpAlaMetLeuGlyAlaValGlu 51

QY 60 GGGTGACTGTGGTCGTGACAGGTGGCTGCAACGAGGGTCCGACAGATGCTGCTCAAG 119

Db 52 GlyProArgTrp-----55

QY 120 AAACAGACGGAGACATCAGCAGTGTCTATGAGATCCGGGAGAAGCTGGGCTCGGGTGCC 179

Db 56 LysGlnAlaGluAspIleArgAspIleTyrAspPheArgAspValLeuGlyThrGlyAla 75

QY 180 TTCTCTGAGGTGATGCTGGCCAGGAAGGGGCTCTGCTCATCTTGTGGCCCTCAAGTGC 239

Db 76 PheSerGluValIleLeuAlaGluAspLysArgThrGlnLysLeuValAlaIleLysCys 95

QY 240 ATTCCCAAGAAAGCACTTCGGGGCAAGGAGGCCCTGGTGGAGAATGAGATCGCGGTACTT 299

Db 96 IleAlaLysGluAlaLeuGluGlyLysGluGlySerMetGluAsnGluIleAlaValLeu 115

QY 300 CGCAGAATCAGCATCCCAACATTGTGGCTCTGGAGGACGTCCATGAGATCCTTCTCAT 359

Db 116 HisLysIleLysHisProAsnIleValAlaLeuAspAspIleTyrGluSerGlyGlyHis 135

QY 360 CTCTACTTGGCGTAGCTGGTAACAGGTGGTGAACCTGTTGACCGCATCATGGAGCGG 419

Db 136 LeuTyrLeuIleMetGlnLeuValSerGlyGlyGluLeuPheAspArgIleValGluLys 155

QY 420 GGCTCCTACACAGAGAAGGACGCCACCTTGTAGGGCAGGTCCCTTGGCGCTGTCTCC 479

Db 156 GlyPheTyrThrGluArgAspAlaSerArgLeuIlePheGlnValLeuAspAlaValLys 175

QY 480 TACCTTCATAGCCTGGGCATCGTGCACCGGACCTCAAGCCCTGAAAACCTCTCTATGCC 539

Db 176 TyrLeuHisAspLeuGlyIleValHisArgAspLeuLysProGluAsnLeuLeuTyrTyr 195

QY 540 ACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTTGGCCTGTCCAAAATACAA--- 596

Db 196 SerLeuAspGluAspSerLysIleMetIleSerAspPheGlyLeuSerLysMetGluAsp 215

QY 597 GCTGGCAACATGCTAGGCACAGCCTGTGGGACCCCGAGGATATGTGGCCCGAGAGCTCCTG 656

Db 216 ProGlySerValLeuSerThrAlaCysGlyThrProGlyTyrValAlaProGluValLeu 235

QY 657 GAGCAGAAACCCTACGGGAAGCCGTAGATGTGTGGCCCTGGGTGTCTATCTCTACATC 716

Db 236 AlaGlnLysProTyrSerLysAlaValAspCysTrpSerIleGlyValIleAlaTyrIle 255

QY 717 CTGCTGTGGGTACCCCCCTTCTATGATGAGAGCGATCCTGAACCTTTCAGCCAGATT 776

Db 256 LeuLeuCysGlyTyrProProPheTyrAspGluAsnAspAlaLysLeuPheGluGlnIle 275

QY 777 CTGAGGGCCAGCTATGAGTTTGACTCCCCCTTTTGGGATGACATCTCAGAATCAGCCAAA 836

Db 276 LeuLysAlaGluTyrGluPheAspSerProTyrTrpAspAspIleSerAspSerAlaLys 295

QY 837 GACTTCATTCGCCACCTTCTGGAACGTGATCCCCAGAGAGGTTTCACTGCCAGCAGGCC 896

Db 296 AspPheIleArgHisLeuMetGluLysAspProGluLysArgPheThrCysGluGlnAla 315

QY 897 CTACAGCATCTTTGGATCTCTGGGGATGCGAGCCTTCGATAGGGACATCCTGGGTTTCTGTC 956

Db 316 LeuGlnHisProTrpIleAlaGlyAspThrAlaLeuAspLysAsnIleHisGlnSerVal 335

QY 957 AGTGAGCAGATCCAGAAGAATTTTGCAGGACCCCACTGGAAGCGTGCAATCAATGCCACA 1016

Db 336 SerGluGlnIleLysLysAsnPheAlaLysSerLysTrpLysGlnAlaPheAsnAlaThr 355

QY 1017 TCATTCCTACGTCACATCCGTAAG-----CTGGGACAAAGCCCGAGGGTGAG 1064

Db 356 AlaValValArgHisMetArgLysLeuGlnLeuGlyThrSerGlnGluGlyGln 373

RESULT 6

US-08-878-989-19

; Sequence 19, Application US/08878989

; Patent No. 5885803

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Hillman, Jennifer L.

; APPLICANT: Corley, Neil C.

; APPLICANT: Guegler, Karl G.

; APPLICANT: Lal, Preeti

; APPLICANT: Goli, Surya K.

; APPLICANT: Shah, Purvi

; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/878,989

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

```

; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0321 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 370 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 790790
US-08-878-989-19

Alignment Scores:
Pred. No.: 1.72e-100 Length: 370
Score: 1184.50 Matches: 220
Percent Similarity: 85.53% Conservative: 52
Best Local Similarity: 69.18% Mismatches: 43
Query Match: 41.24% Indels: 3
DB: 2 Gaps: 2

US-10-032-254A-1 (1-1554) x US-08-878-989-19 (1-370)

QY 120 AAACAGACGGAGACATCAGCAGTGTCTATGAGATCCGGGAGAGCTGGGCTCGGGTGCC 179
Db 11 LysGlnAlaGluAspIleArgAspIleTyrAspPheArgAspValLeuGlyThrGlyAla 30
QY 180 TTCTCTGAGGTATGCTGGCCAGGAAAGGGGCTCTGCTCATCTTTGTGGCCCTCAAGTGC 239
Db 31 PheSerGluValIleLeuAlaGluAspLysArgThrGlnLysLeuValAlaIleLysCys 50
QY 240 ATTCCCAAGAAAGCACTTCGGGGCAAGAGGCCCTGGTGGAGAATGAGATCGGGTACTT 299
Db 51 IleAlaLysGluAlaLeuGluGlyLysGluGlySerMetGluAsnGluIleAlaValLeu 70
QY 300 CGCAGAATCAGCCATCCCAACATTGTGGCTCTGGAGGACGTCCATGAGATCCTTCTCAT 359
Db 71 HisLysIleLysHisProAsnIleValAlaLeuAspAspIleTyrGluSerGlyGlyHis 90
QY 360 CTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAACCTGTTTACCGCATCATGGAGCGG 419
Db 91 LeuTyrLeuIleMetGlnLeuValSerGlyGlyGluLeuPheAspArgIleValGluLys 110
QY 420 GGCTCCTACACAGAGAAGGACGCCAGCCACCTTGTAGGGCAGGTCTTGGCGCTGTCTCC 479
Db 111 GlyPheTyrThrGluArgAspAlaSerArgLeuIlePheGlnValLeuAspAlaValLys 130
QY 480 TACCTTCATAGCCTGGCATCGTGCACCGGGACCTCAAGCCTGAAACCTCCTCTATGCC 539
Db 131 TyrLeuHisAspLeuGlyIleValHisArgAspLeuLysProGluAsnLeuTyrTyr 150
QY 540 ACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTGGCCTGTCCAAATACAA --- 596
Db 151 SerLeuAspGluAspSerLysIleMetIleSerAspPheGlyLeuSerLysMetGluAsp 170
QY 597 GCTGGCAACATGCTAGGCACAGCCTGTGGACCCAGGATATGTGGCCCAAGAGCTCCTG 656
Db 171 ProGlySerValLeuSerThrAlaCysGlyThrProGlyTyrValAlaProGluValLeu 190
QY 657 GAGCAGAAACCCTACGGGAAGCGCGTAGATGTGTGGCCCTGGGTGTCTATCTCTACATC 716
Db 191 AlaGlnLysProTyrSerLysAlaValAspCysTrpSerIleGlyValIleAlaTyrIle 210
QY 717 CTGCTGTGTGGGTACCCCTTCTATGATGAGAGCGATCCTGAACTCTTACGCCAGATT 776
Db 211 LeuLeuCysGlyTyrProProPheTyrAspGluAsnAspAlaLysLeuPheGluGlnIle 230

; 777 CTGAGGGCCAGCTATGAGTTTGACTCCCTTTTGGGATGACATCTCAGAAATCAGCCAAA 836
; 231 LeuLysAlaGluTyrGluPheAspSerProTyrTrpAspAspIleSerAspSerAlaLys 250
; 837 GACTTCATTGCGCCACCTTCTGGAAACGTGATCCCCAGAAAGAGGTTTACCTGCCAGCAGGCC 896
; 251 AspPheIleArgHisLeuMetGluLysAspProGluLysArgPheThrCysGluGlnAla 270
; 897 CTACAGCATCTTTGGATCTCTGGGGATGCAGCCCTTCGATAGGGACATCTCTGGGTTCTGTC 956
; 271 LeuGlnHisProTyrIleAlaGlyAspThrAlaLeuAspLysAsnIleHisGlnSerVal 290
; 957 AGTGACGAGATCCAGAAAGAAATTTTCCAGGACCCACTGGAAGCGTGCATTTCAATGCCACA 1016
; 291 SerGluGlnIleLysLysAsnPheAlaLysSerLysTrpLysGlnAlaPheAsnAlaThr 310
; 1017 TCATTCCTACGTACATCCGTAAG-----CTGGGACAAAGCCCAAGAGGTTGAG 1064
; 311 AlaValValArgHisMetArgLysLeuGlnLeuGlyThrSerGlnGluGlyGln 328

RESULT 7
US-09-272-796-19
; Sequence 19, Application US/09272796
; Patent No. 6207148
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl G.
; APPLICANT: Lal, Preeti
; APPLICANT: Goli, Surya K.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; TITLE OF INVENTION: KINASES
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/272,796
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/878,989
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0321 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 370 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 790790
US-09-272-796-19
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Db 211 LeuLeuCysGlyTyrProPheTyrAspGluAsnAspAlaLysLeuPheGluGlnIle 230

QY 777 CTGAGGGCCAGCTATGAGTTTGACTCCCTTTTGGGATGACATCTCAGAAATCAGCCAAA 836  
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Db 231 LeuLysAlaGluTyrGluPheAspSerProTyrTrpAspAspIleSerAspSerAlaLys 250

QY 837 GACTTCATTGCCACCTTCTGGAACGTATCCCCAGAAGAGGTTACCTGCCAGAGGCC 896  
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Db 251 AspPheIleArgHisLeuMetGluLysAspProGluLysArgPheThrCysGluGlnAla 270

QY 897 CTACAGCATCTTTGGATCTCTGGGGATGCAGCCTTCGATAGGGACATCCTGGGTTCTGTC 956  
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Db 271 LeuGlnHisProTrpIleAlaGlyAspThrAlaLeuAspLysAsnIleHisGlnSerVal 290

QY 957 AGTGAGCAGATCCAGAAAGATTTTGCCAGGACCCCACTGGAAGCGTGCAATCAATGCCACA 1016  
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Db 291 SerGluGlnIleLysLysAsnPheAlaLysSerLysTrpLysGlnAlaPheAsnAlaThr 310

QY 1017 TCATTCCCTACGTCCATCCGTAAG-----CTGGGACAAAGCCCCAGAGGGTGAG 1064  
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Db 311 AlaValValArgHisMetArgLysLeuGlnLeuGlyThrSerGlnGluGlyGln 328

RESULT 9

US-09-538-092-1314

; Sequence 1314, Application US/09538092

; Patent No. 6753314

; GENERAL INFORMATION:

; APPLICANT: Giot, Loic

; APPLICANT: Mansfield, Traci A.

; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same

; FILE REFERENCE: 15966-542

; CURRENT APPLICATION NUMBER: US/09/538,092

; PRIOR APPLICATION NUMBER: 2000-03-29

; PRIOR FILING DATE: 1999-04-01

; PRIOR APPLICATION NUMBER: 60/127,352

; PRIOR FILING DATE: 1999-04-01

; PRIOR APPLICATION NUMBER: 60/178,965

; PRIOR FILING DATE: 2000-02-01

; NUMBER OF SEQ ID NOS: 1387

; SOFTWARE: CuraPatSeqformatter Version 0.9

; SEQ ID NO 1314

; LENGTH: 370

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc\_feature

; LOCATION: (0)...(0)

; OTHER INFORMATION: Polypeptide Accession Number Q14012

US-09-538-092-1314

Alignment Scores:

Pred. No.:	1.72e-100	Length:	370
Score:	1184.50	Matches:	220
Percent Similarity:	85.53%	Conservative:	52
Best Local Similarity:	69.18%	Mismatches:	43
Query Match:	41.24%	Indels:	3
DB:	4	Gaps:	2

US-10-032-254A-1 (1-1554) x US-09-538-092-1314 (1-370)

QY 120 AAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAAGCTGGGCTCGGGTGCC 179  
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Db 11 LysGlnAlaGluAspIleArgAspIleTyrAspPheArgAspValLeuGlyThrGlyAla 30

QY 180 TTCTCTGAGGTGATGTGGCCAGGAAAGGGCTCTGCTCATCTTTGTGGCCCTCAAGTGC 239  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 31 PheSerGluValIleLeuAlaGluAspLysArgThrGlnLysLeuValAlaIleLysCys 50  
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QY 240 ATTCCCAAGAAAGCACTTCGGGGCAAGGAGGCCCTGTGGAGAATGAGATCGCGGTACTT 299  
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Db 51 IleAlaLysGluAlaLeuGluGlyLysGluGlySerMetGluAsnGluIleAlaValLeu 70  
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QY 300 CGCAGAATCAGCCATCCCAACATTTGTGGCTCTGGAGGACGTCATGAGAGTCCTTCTCAT 359  
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Db 71 HisLysIleLysHisProAsnIleValAlaLeuAspAspIleTyrGluSerGlyGlyHis 90

QY 360 CTCTACTTTGGCCATGGAGCTGTAACAGGTGGTGAACCTGTTTACCGCATCATGGAGCGG 419  
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Db 91 LeuTyrLeuIleMetGlnLeuValSerGlyGlyGluLeuPheAspArgIleValGluLys 110

QY 420 GGCTCCTACACAGAGAAAGGACCCAGCCACCTTGTAGGGCAGGTCTCTGGCGTGTCTCC 479  
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Db 111 GlyPheTyrThrGluArgAspAlaSerArgLeuIlePheGlnValLeuAspAlaValLys 130

QY 480 TACCTTCATAGCCTGGGCATGTGCACCGGGACCTCAAGCCTGAAACCTCCTCTATGCC 539  
||||:||||| ||||:||||| ||||:||||| ||||:||||| ||||:||||| ||||:|||||

Db 131 TyrLeuHisAspLeuGlyIleValHisArgAspLeuLysProGluAsnLeuTyrTyr 150

QY 540 ACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTTGGCCTGTCCAAAATACAA --- 596  
::: ||||:||||| ||||:||||| ||||:||||| ||||:||||| ||||:||||| ||||:|||||

Db 151 SerLeuAspGluAspSerLysIleMetIleSerAspPheGlyLeuSerLysMetGluAsp 170

QY 597 GCTGGCAACATGTAGGCACAGCCTGTGGACCCCGAGGATATGTGGCCCTCATCTCTACATC 656  
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Db 171 ProGlySerValLeuSerThrAlaCysGlyThrProGlyTyrValAlaProGluValLeu 190

QY 657 GAGCAGAAACCCCTACCGGAAGGCCGTAGATGTGTGGGCCCTGGGTGTCTATCTCTACATC 716  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 191 AlaGlnLysProTyrSerLysAlaValAspCysTrpSerIleGlyValIleAlaTyrIle 210

QY 717 CTGCTGTGTGGGTACCCCTTCTATGATGAGAGCGATCCTGAACCTCTTCAGCCAGATT 776  
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Db 211 LeuLeuCysGlyTyrProPheTyrAspGluAsnAspAlaLysLeuPheGluGlnIle 230

QY 777 CTGAGGCCAGCTATGAGTTTGACTCCCTTCTTGGGATGACATCTCAGAAATCAGCCAAA 836  
||||:||||| ||||:||||| ||||:||||| ||||:||||| ||||:||||| ||||:|||||

Db 231 LeuLysAlaGluTyrGluPheAspSerProTyrTrpAspAspIleSerAspSerAlaLys 250

QY 837 GACTTCATTGCCACCTTCTGGAACGTGATCCCGAGAGAGGTTTCACTTCCAGCAGGCC 896  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 251 AspPheIleArgHisLeuMetGluLysAspProGluLysArgPheThrCysGluGlnAla 270

QY 897 CTACAGCATCTTTGGATCTCTGGGGATGCAGCCTTCGATAGGGACATCCTGGGTTCTGTC 956  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 271 LeuGlnHisProTrpIleAlaGlyAspThrAlaLeuAspLysAsnIleHisGlnSerVal 290

QY 957 AGTGAGCAGATCCAGAAAGATTTTGCCAGGACCCCACTGGAAGCGTGCAATCAATGCCACA 1016  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 291 SerGluGlnIleLysLysAsnPheAlaLysSerLysTrpLysGlnAlaPheAsnAlaThr 310

QY 1017 TCATTCCCTACGTCCATCCGTAAG-----CTGGGACAAAGCCCCAGAGGGTGAG 1064  
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Db 311 AlaValValArgHisMetArgLysLeuGlnLeuGlyThrSerGlnGluGlyGln 328

RESULT 10

US-09-733-388-2

; Sequence 2, Application US/09733388

; Patent No. 6602698

; GENERAL INFORMATION:

; APPLICANT: Donoho, Greg

; APPLICANT: Scoville, John

; APPLICANT: Turner, C. Alexander Jr.

; APPLICANT: Friedrich, Glenn

; APPLICANT: Zambrowicz, Brian

; APPLICANT: Abuin, Alejandro

; APPLICANT: Sands, Arthur T.

; TITLE OF INVENTION: No. 6602698el Human Kinase Proteins and

; FILE REFERENCE: LEX-0103-USA

; CURRENT APPLICATION NUMBER: US/09/733,388

; CURRENT FILING DATE: 2000-12-07

; PRIOR APPLICATION NUMBER: US 60/169,428

; PRIOR FILING DATE: 1999-12-07

; NUMBER OF SEQ ID NOS: 5

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2

; LENGTH: 385

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-733-388-2

Alignment Scores:
Pred. No.:      1.82e-99      Length:      385
Score:          1173.50      Matches:    216
Percent Similarity: 85.09%      Conservative: 58
Best Local Similarity: 67.08%      Mismatches: 45
Query Match:    40.86%      Indels:    3
DB:              4              Gaps:    2

US-10-032-254A-1 (1-1554) x US-09-733-388-2 (1-385)

QY 117 AAGAAACAGACGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAGCTGGGCTCGGT 176
Db 13 LysLysGlnAlaGluAspIleLysLysIlePheGluPheLysGluThrLeuGlyThrGly 32
QY 177 GCCTTCTCTGAGTGTATGCTGGCCAGGAAAGGGGCTCTGCTCATCTTGTGGCCCTCAAG 236
Db 33 AlaPheSerGluValValLeuAlaGluGluLysAlaThrGlyLysLeuPheAlaValLys 52
QY 237 TGCATTCCCAAGAACGACTTCGGGGCAAGGAGCCCTGGTGGAGATGAGATCGCGGTA 296
Db 53 CysIleProLysLysAlaLeuLysGlyLysGluSerSerIleGluAsnGluIleAlaVal 72
QY 297 CTTGCGAGATACCCATCCCAACATTGTGGCTCTGGAGACGTCCATGAGAGTCTTCT 356
Db 73 LeuArgLysIleLysHisGluAsnIleValAlaLeuGluAspIleTyrGluSerProAsn 92
QY 357 CATCTCTACTTGGCCATGGAGCTGGTAACAGTGGTGAACCTGTTTGACCGCATCATGGAG 416
Db 93 HisLeuTyrLeuValMetGlnLeuValSerGlyGlyGluLeuPheAspArgIleValGlu 112
QY 417 CGGGGCTCCTACAGAGAGGACGCCACCTTGTAGGGCAGGTCTTGGCGGTGTC 476
Db 113 LysGlyPheTyrThrGluLysAspAlaSerThrLeuIleArgGlnValLeuAspAlaVal 132
QY 477 TCCTACCTTCATAGCCTGGGCATCGTGACCGGACCTCAAGCCTGAAAACTCCTCTAT 536
Db 133 TyrTyrLeuHisArgMetGlyIleValHisArgAspLeuLysProGluAsnLeuTyr 152
QY 537 GCCACACCTTTTGAGGACTCCAAGATCATGTCTCTGACTTTGGCCTGTGCCAAATACAA 596
Db 153 TyrSerGlnAspGluGluSerLysIleMetIleSerAspPheGlyLeuSerLysMetGlu 172
QY 597 GCT--GGCAACATGCTAGGCACAGCCTGTGGACCCCGAGGATATGTGGCCCGCAGAGTC 653
Db 173 GlyLysGlyAspValMetSerThrAlaCysGlyThrProGlyTyrValAlaProGluVal 192
QY 654 CTGGAGCAGAAACCTTACGGGAAGCCGTAGATGTGTGGGCCCTGGGTGTCTATCCTCTAC 713
Db 193 LeuAlaGlnLysProTyrSerLysAlaValAspCysTrpSerIleGlyValIleAlaTyr 212
QY 714 ATCCTGCTGTGGGTACCCCTTCTATGATGAGAGCGATCCTGAACTCTTCAGCCAG 773
Db 213 IleLeuLeuCysGlyTyrProProPheTyrAspGluAsnAspSerLysLeuPheGluGln 232
QY 774 ATTCTGAGGCGCAGCTATGAGTTTGACTCCCTCTTGGGATGACATCTCAGAAATCAGCC 833
Db 233 IleLeuLysAlaGluTyrGluPheAspSerProTyrTrpAspAspIleSerAspSerAla 252
QY 834 AAAGACTTCATTGCCACCTTCTGGAACGTGATCCCGAGAGAGGTTCACTGCCAGCAG 893
Db 253 LysAspPheIleArgAsnLeuMetGluLysAspProAsnLysArgTyrThrCysGluGln 272
QY 894 GCCCTACAGCATCTTTGGATCTCTGGGGATGCAGCCTTCGATAGGGACATCCTGGGTTCT 953
Db 273 AlaAlaArgHisProTrpIleAlaGlyAspThrAlaLeuAsnLysAsnIleHisGluSer 292
QY 954 GTCAGTGAGCATCCAGAAAGAAATTTTGCAGGACCCACTGGAAGCGGTGCATTCATGCC 1013
Db 293 ValSerAlaGlnIleArgLysAsnPheAlaLysSerLysTrpArgGlnAlaPheAsnAla 312

QY 1014 ACATCATTCCTACGTCACTCCGTAAG-----CTGGGACAAAGCCCAGAGGTGAGGAG 1067
Db 313 ThrAlaValValArgHisMetArgLysLeuHisLeuGlySerSerLeuAspSerSerAsn 332
QY 1068 GCCTCC 1073
Db 333 AlaSer 334

RESULT 11
US-10-446-175-2
; Sequence 2, Application US/10446175
; Patent No. 6806073
; GENERAL INFORMATION:
; APPLICANT: Donoho, Greg
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Abuin, Alejandro
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6806073el Human Kinase Proteins and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0103-USA
; CURRENT APPLICATION NUMBER: US/10/446,175
; CURRENT FILING DATE: 2003-05-27
; PRIOR APPLICATION NUMBER: US/09/733,388
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,428
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-446-175-2

Alignment Scores:
Pred. No.:      1.82e-99      Length:      385
Score:          1173.50      Matches:    216
Percent Similarity: 85.09%      Conservative: 58
Best Local Similarity: 67.08%      Mismatches: 45
Query Match:    40.86%      Indels:    3
DB:              4              Gaps:    2

US-10-032-254A-1 (1-1554) x US-10-446-175-2 (1-385)

QY 117 AAGAAACAGACGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAGCTGGGCTCGGT 176
Db 13 LysLysGlnAlaGluAspIleLysLysIlePheGluPheLysGluThrLeuGlyThrGly 32
QY 177 GCCTTCTCTGAGTGTATGCTGGCCAGGAAAGGGGCTCTGCTCATCTTGTGGCCCTCAAG 236
Db 33 AlaPheSerGluValValLeuAlaGluGluLysAlaThrGlyLysLeuPheAlaValLys 52
QY 237 TGCATTCCCAAGAAAGCATTTCGGGGCAAGGAGCCCTGGTGGAGATGAGATCGCGGTA 296
Db 53 CysIleProLysLysAlaLeuLysGlyLysGluSerSerIleGluAsnGluIleAlaVal 72
QY 297 CTTGCGAGATACCCATCCCAACATTGTGGCTCTGGAGACGTCCATGAGAGTCTTCT 356
Db 73 LeuArgLysIleLysHisGluAsnIleValAlaLeuGluAspIleTyrGluSerProAsn 92
QY 357 CATCTCTACTTGGCCATGGAGCTGGTAACAGTGGTGAACCTGTTTGACCGCATCATGGAG 416
Db 93 HisLeuTyrLeuValMetGlnLeuValSerGlyGlyGluLeuPheAspArgIleValGlu 112
QY 417 CGGGGCTCCTACAGAGAGGACGCCACCTTGTAGGGCAGGTCTTGGCGGTGTC 476
Db 113 LysGlyPheTyrThrGluLysAspAlaSerThrLeuIleArgGlnValLeuAspAlaVal 132
QY 477 TCCTACCTTCATAGCCTGGGCATCGTGACCGGACCTCAAGCCTGAAAACTCCTCTAT 536
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Db 133 TyrTyrLeuHisArgMetGlyIleValHisArgAspLeuLysProGluAsnLeuLeuTyr 152  
QY 537 GCCACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTGGCCTGTCCAAATACAA 596  
Db 153 TyrSerGlnAspGluSerLysIleMetIleSerAspPheGlyLeuSerLysMetGlu 172  
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QY 654 CTGGAGCAGAAACCTTACGGGAAGCGGTAGATGTGTGGGCCCTGGGTGTCAATCTCCTAC 713  
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QY 714 ATCCTGCTGTGTGGGTACCCCCCTTCTATGATGAGAGCGATCCTGAACTCTTCAGCCAG 773  
Db 213 IleLeuLeuCysGlyTyrProProPheTyrAspGluAsnAspSerLysLeuPheGluGln 232  
QY 774 ATTCTGAGGCGCAGCTATGAGTTTGACTCCCCCTTTTGGGATGACATCTCAGAATCAGCC 833  
Db 233 IleLeuLysAlaGluTyrGluPheAspSerProTyrTrpAspAspIleSerAspSerAla 252  
QY 834 AAAGACTTCATTGCCACCTTCTTGGAACTGATCCCCCAGAGAGGTTACCTGCCAGCAG 893  
Db 253 LysAspPheIleArgAsnLeuMetGluLysAspProAsnLysArgTyrThrCysGluGln 272  
QY 894 GCCCTACAGCATCTTTGGATCTCTGGGGATGCGAGCCTTCGATAGGACATCCTGGGTTCT 953  
Db 273 AlaAlaArgHisProTrpIleAlaGlyAspThrAlaLeuAsnLysAsnIleHisGluSer 292  
QY 954 GTCAGTGAGCATCCAGAAAGAAATTTGCCAGGACCCACTGGAAGCGTGCATTCATGCC 1013  
Db 293 ValSerAlaGlnIleArgLysAsnPheAlaLysSerLysTrpArgGlnAlaPheAsnAla 312  
QY 1014 ACATCATTCCTACGTCACATCCGTAAG-----CTGGGACAAAGCCAGAGGGTGAGGAG 1067  
Db 313 ThrAlaValValArgHisMetArgLysLeuHisLeuGlySerSerLeuAspSerSerAsn 332  
QY 1068 GCCTCC 1073  
Db 333 AlaSer 334

RESULT 12  
US-09-579-664B-10  
; Sequence 10, Application US/09579664B  
; Patent No. 6514719  
; GENERAL INFORMATION:  
; APPLICANT: Immunex Corporation  
; APPLICANT: Bird, Timothy A.  
; APPLICANT: Virca, G. Duke  
; APPLICANT: Martin, Unja  
; APPLICANT: Anderson, Dirk M.  
; TITLE OF INVENTION: NOVEL MURINE AND HUMAN KINASES  
; FILE REFERENCE: 2923-A  
; CURRENT APPLICATION NUMBER: US/09/579,664B  
; CURRENT FILING DATE: 2000-05-26  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 355  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-579-664B-10

Alignment Scores:  
Pred. No.: 4.08e-99 Length: 355  
Score: 1169.50 Matches: 215  
Percent Similarity: 84.78% Conservative: 58  
Best Local Similarity: 66.77% Mismatches: 46  
Query Match: 40.72% Indels: 3  
DB: 4 Gaps: 2

US-10-032-254A-1 (1-1554) x US-09-579-664B-10 (1-355)  
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QY 177 GCCTTCTCTGAGGTGATGTGGCCCGCCAGAAAGGGGCTCTGCTCATCTTGTGGCCCTCAAG 236  
Db 33 AlaPheSerGluValValLeuAlaGluGluLysAlaThrGlyLysLeuPheAlaValLys 52  
QY 237 TGCATTCCCAAGAAAGCACTTCGGGGCAAGGAGGCCCTGTGTGAGAAATGAGATCGCGGTA 296  
Db 53 CysIleProLysLysAlaLeuLysGlyLysGluSerSerIleGluAsnGluIleAlaVal 72  
QY 297 CTTTCGAGAATCAGCCATCCCAACATTGTGGCTCTGAGGAGCTCCATGAGAGTCCTTCT 356  
Db 73 LeuArgLysIleLysHisGluAsnIleValAlaLeuGluAspIleTyrGluSerProAsn 92  
QY 357 CATCTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAACCTGTTGACCCGATCATGGAG 416  
Db 93 HisLeuTyrLeuValMetGlnLeuValSerGlyGlyGluLeuPheAspArgIleValGlu 112  
QY 417 CGGGCTCCTACACAGAGAAGACGCCAGCCACCTTGTAGGGCAGGTCTTGGCGCTGTC 476  
Db 113 LysGlyPheTyrThrGluLysAspAlaSerThrLeuIleArgGlnValLeuAspAlaVal 132  
QY 477 TCCTACCTTCATAGCCTGGGATCGTGCACCGGGACCTCAAGCTGAAAACCTCCTCTAT 536  
Db 133 TyrTyrLeuHisArgMetGlyIleValHisArgAspLeuLysProGluAsnLeuLeuTyr 152  
QY 537 GCCACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTGGCTGTCCAAAATACAA 596  
Db 153 TyrSerGlnAspGluGluSerLysIleMetIleSerAspPheGlyLeuSerLysMetGlu 172  
QY 597 GCT---GGCAACATGCTAGGCACAGCCTGTGGGACCCCGAGGATATGTGGCCCGCAGAGCTC 653  
Db 173 GlyLysGlyAspValMetSerThrAlaCysGlyThrProGlyTyrValAlaProGluVal 192  
QY 654 CTGGAGCAGAAACCCCTACGGGAAGCGCGTAGATGTGTGGGCCCTGGGTGTCTCCTAC 713  
Db 193 LeuAlaGlnLysProTyrSerLysAlaValAspCysTrpSerIleGlyValIleAlaTyr 212  
QY 714 ATCCTGCTGTGTGGGTACCCCTTCTATGATGAGAGCGATCCTGAACTCTTCAGCCAG 773  
Db 213 IleLeuLeuCysGlyTyrProProPheTyrAspGluAsnAspSerLysLeuPheGluGln 232  
QY 774 ATTCTGAGGCGCAGCTATGAGTTTGACTCCCCCTTTTGGGATGACATCTCAGAATCAGCC 833  
Db 233 IleLeuLysAlaGluTyrGluPheAspSerProTyrTrpAspAspIleSerAspSerAla 252  
QY 834 AAAGACTTCATTGCCACCTTCTTGGAACTGATCCCCCAGAGAGGTTACCTGCCAGCAG 893  
Db 253 LysAspPheIleArgAsnLeuMetGluLysAspProAsnLysArgTyrThrCysGluGln 272  
QY 894 GCCCTACAGCATCTTTGGATCTCTGGGGATGCGAGCCTTCGATAGGACATCCTGGGTTCT 953  
Db 273 AlaAlaArgHisProTrpIleAlaGlyAspThrAlaLeuSerLysAsnIleHisGluSer 292  
QY 954 GTCAGTGAGCATCCAGAAAGAAATTTGCCAGGACCCACTGGAAGCGTGCATTCATGCC 1013  
Db 293 ValSerAlaGlnIleArgLysAsnPheAlaLysSerLysTrpArgGlnAlaPheAsnAla 312  
QY 1014 ACATCATTCCTACGTCACATCCGTAAG-----CTGGGACAAAGCCAGAGGGTGAGGAG 1067  
Db 313 ThrAlaValValArgHisMetArgLysLeuHisLeuGlySerSerLeuAspSerSerAsn 332  
QY 1068 GCCTCC 1073  
Db 333 AlaSer 334

RESULT 13  
US-10-355-975A-10  
; Sequence 10, Application US/10355975A

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; Patent No. 6759223
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Bird, Timothy A.
; APPLICANT: Virca, G. Duke
; APPLICANT: Martin, Unja
; APPLICANT: Anderson, Dirk M.
; TITLE OF INVENTION: CALCIUM/CALMODULIN-DEPENDENT KINASE
; FILE REFERENCE: 2923-B
; CURRENT APPLICATION NUMBER: US/10/355,975A
; CURRENT FILING DATE: 2003-01-30
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 355
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-355-975A-10

Alignment Scores:
Pred. No.: 4 08e-99 Length: 355
Score: 1169.50 Matches: 215
Percent Similarity: 84.78% Conservative: 58
Best Local Similarity: 66.77% Mismatches: 46
Query Match: 40.72% Indels: 3
DB: 4 Gaps: 2

US-10-032-254A-1 (1-1554) x US-10-355-975A-10 (1-355)

QY 117 AAGAAACAGACGGAGACATCAGCAGTGTCTATGATCCGGGAGAGCTGGGCTCGGT 176
Db 13 LysLysGlnAlaGluAspIleLysLysIlePheGluPheLysGluThrLeuGlyThrGly 32

QY 177 GCCTTCTCTGAGGTGATGCTGGCCAGGAAAGGGCTCTGCTCATCTTGTGGCCCTCAAG 236
Db 33 AlaPheSerGluValValLeuAlaGluLysAlaThrGlyLysLeuPheAlaValLys 52

QY 237 TGCATTCCCAAGAAAGCACTTCGGGGCAAGGAGGCGCTTGGAGAAATGAGATCGCGGTA 296
Db 53 CysIleProLysLysAlaLeuLysGlyLysGluSerSerIleGluAsnGluIleAlaVal 72

QY 297 CTTCGCAGAAATCAGCCATCCCAACATTTGTGGCTCTGGAGGACGTCCATGAGAGTCTTCT 356
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QY 357 CATCTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAACCTGTTGACCGCATCATGGAG 416
Db 93 HisLeuTyrLeuValMetGlnLeuValSerGlyGlyGluLeuPheAspArgIleValGlu 112

QY 417 CGGGGCTCCTACAGAGAAAGGACGCCACCTTGTAGGCGAGGTCTTGGGCTGTC 476
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QY 477 TCCTACCTTCATAGCTGGGCATCGTGACCCGGGACCTCAAGCCTGAAAACCTCTCTAT 536
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QY 537 GCCACACCTTTTGAGGACTCCAAGATCATGCTCTCTGACTTTGGCCCTGTCCAAATACAA 596
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QY 597 GCT--GGCAACATGCTAGGCACAGCCTGTGGGACCCAGGATATGTGGCCCCAGAGCTC 653
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Db 332 AlaSer 333

RESULT 15  
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; Sequence 4, Application US/10446175  
; Patent No. 6806073  
; GENERAL INFORMATION:  
; APPLICANT: Donoho, Greg  
; APPLICANT: Scoville, John  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Abuin, Alejandro  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: No. 6806073el Human Kinase Proteins and  
; TITLE OF INVENTION: Polynucleotides Encoding the Same  
; FILE REFERENCE: LEX-0103-USA  
; CURRENT APPLICATION NUMBER: US/10/446,175  
; CURRENT FILING DATE: 2003-05-27

; PRIOR APPLICATION NUMBER: US/09/733,388  
; PRIOR FILING DATE: 2000-12-07  
; PRIOR APPLICATION NUMBER: US 60/169,428  
; PRIOR FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 356  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-446-175-4  
  
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Search completed: June 6, 2005, 12:11:48  
Job time : 55 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 6, 2005, 11:58:41 ; Search time 822 Seconds  
(without alignments)  
1307.023 Million cell updates/sec

Title: US-10-032-254A-1  
Perfect score: 2872  
Sequence: 1 gttgcggagtcctccactc.....caaaaaaaaaaaaaaaaaaa 1554

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1465611 seqs, 345679903 residues

Total number of hits satisfying chosen parameters: 2931222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-Q=/cgn2\_1/USPTO\_spool\_p/US10032254/runat\_02062005\_131021\_3713/app query.fasta\_1.1735  
-DB=Published Applications AA -QFMT=fastan -SUFFIX=rapb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62  
-TRANS=human40.cdi -LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZ=500 -MINLEN=0  
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-NCPU=6 -ICPU=3 -NO\_MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100  
-LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
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Database : Published Applications AA:

- 1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pép:\*
- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pép:\*
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- 20: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pép:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result % Query

No.	Score	Match	Length	DB	ID	Description
1	1799.5	62.7	484	15	US-10-425-114-54130	Sequence 54130, A
2	1625	56.6	343	10	US-09-769-970-5	Sequence 5, Appli
3	1625	56.6	343	17	US-10-948-518-89	Sequence 89, Appl
4	1184.5	41.2	332	16	US-10-664-421-13	Sequence 13, Appl
5	1184.5	41.2	370	9	US-09-817-181-4	Sequence 4, Appli
6	1184.5	41.2	370	10	US-09-769-970-19	Sequence 19, Appl
7	1184.5	41.2	370	14	US-10-142-356-7	Sequence 7, Appli
8	1184.5	41.2	370	14	US-10-300-828-4	Sequence 4, Appli
9	1184.5	41.2	370	14	US-10-090-002-4	Sequence 4, Appli
10	1184.5	41.2	370	14	US-10-204-041-10	Sequence 10, Appl
11	1184.5	41.2	370	16	US-10-649-400-6	Sequence 6, Appli
12	1182.5	41.2	317	10	US-09-935-464-36	Sequence 36, Appl
13	1182.5	41.2	317	14	US-10-125-835-36	Sequence 36, Appl
14	1176.5	41.0	326	16	US-10-664-421-55	Sequence 55, Appl
15	1173.5	40.9	355	15	US-10-258-106-11	Sequence 11, Appl
16	1173.5	40.9	357	14	US-10-024-036B-2	Sequence 2, Appli
17	1173.5	40.9	357	15	US-10-258-106-2	Sequence 2, Appli
18	1173.5	40.9	385	10	US-09-733-388-2	Sequence 2, Appli
19	1173.5	40.9	385	15	US-10-446-175-2	Sequence 2, Appli
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21	1169.5	40.7	355	14	US-10-355-975-10	Sequence 10, Appl
22	1157	40.3	356	10	US-09-733-388-4	Sequence 4, Appli
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26	1065	37.1	460	14	US-10-125-835-3	Sequence 3, Appli
27	1065	37.1	476	9	US-09-960-643-2	Sequence 2, Appli
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29	1065	37.1	476	14	US-10-125-835-5	Sequence 5, Appli
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31	1017.5	35.4	326	9	US-09-817-181-2	Sequence 2, Appli
32	1017.5	35.4	326	14	US-10-300-828-2	Sequence 2, Appli
33	1017.5	35.4	326	14	US-10-090-002-2	Sequence 2, Appli
34	874.5	30.4	298	15	US-10-220-120-240	Sequence 240, App
35	874.5	30.4	310	15	US-10-369-493-5955	Sequence 5955, Ap
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37	869.5	30.3	280	14	US-10-175-042-16	Sequence 16, Appl
38	762	26.5	265	9	US-09-764-868-814	Sequence 814, App
39	762	26.5	265	11	US-09-764-875-1036	Sequence 1036, Ap
40	730	25.4	473	14	US-10-320-351-15	Sequence 15, Appl
41	730	25.4	473	15	US-10-116-275-153	Sequence 153, App
42	725	25.2	501	9	US-09-734-030-2	Sequence 2, Appli
43	725	25.2	501	9	US-09-797-039-2	Sequence 2, Appli
44	725	25.2	501	13	US-10-153-921-2	Sequence 2, Appli
45	725	25.2	501	14	US-10-170-789-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1  
US-10-425-114-54130  
; Sequence 54130, Application US/10425114  
; Publication No. US20040034888A1  
; GENERAL INFORMATION:  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Screen, Steven E  
; APPLICANT: Tabaska, Jack E  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(5313)B  
; CURRENT APPLICATION NUMBER: US/10/425,114  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 73128  
; SEQ ID NO 54130  
; LENGTH: 484  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:



; OTHER INFORMATION: Clone ID: LIB4653-002-F12\_FLI.pep  
US-10-425-114-54130

Alignment Scores:

Pred. No.: 1.21e-134 Length: 484  
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Best Local Similarity: 77.94% Mismatches: 63  
Query Match: 62.66% Indels: 35  
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QY 159 GAGAAAGTGGGCTCGGGTGCCTTCTCTGAGGTGATGCTGGCCAGGAAAGGGGCTCTGCT 218  
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QY 219 CATCTTGTGGCCCTCAAGTGCATTCCCAAGAAAGCACTTCGGGGCAAGGAGGCCCTGGTG 278  
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QY 279 GAGAAATGAGATCGCGGTACTTCGCAGAAATCAGCCATCCCAACATTGTGGTCTCTGGAGGAC 338  
Db 64 GluAsnGluIleAlaValLeuArgArgIleSerHisProAsnIleValAlaLeuGluAsp 83  
QY 339 GTCCATGAGAGTCCTTCTCATCTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAAC TG 398  
Db 84 ValHisGluSerProSerHisLeuTyrLeuAlaMetGluLeuValThrGlyGlyGluLeu 103  
QY 399 TTTGACCGCATCATGAGGGGGCTCCTACACAGAGAAGGACGCCAGCCACCTTGTAGGG 458  
Db 104 PheAspArgIleMetGluArgGlySerTyrThrGluLysAspAlaSerHisLeuValGly 123  
QY 459 CAGGTCTTGGCGCTGCTCCTACCTTATAGCCTGGGCATCGTGACCCGGGACCTCAAG 518  
Db 124 GlnValLeuGlyAlaValSerTyrLeuHisSerLeuGlyIleValHisArgAspLeuLys 143  
QY 519 CCTGAAACCTCCTCTATGCCACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTT 578  
Db 144 ProGluAsnLeuLeuTyrAlaThrProPheGluAspSerLysIleMetValSerAspPhe 163  
QY 579 GGCCTGTCCAAAATACAGCTGGCAACATGCTAGGCACAGCCTGTGGGACCCCGAGGATAT 638  
Db 164 GlyLeuSerLysIleGlnAlaGlyAsnMetLeuGlyThrAlaCysGlyThrProGlyTyr 183  
QY 639 GTGGCCCCAGAGCTCCTGAGCAGAAACCCCTACGGGAAGGCCGTAGATGTGGGCCCTG 698  
Db 184 ValAlaProGluLeuLeuGluGlnLysProTyrGlyLysAlaValAspValTrpAlaLeu 203  
QY 699 GGTGTATCTCTACATCCTGCTGTGTGGGTACCCCCCTTCTATGATGAGAGCGATCCT 758  
Db 204 GlyValIleSerTyrIleLeuLeuCysGlyTyrProProPheTyrAspGluSerAspPro 223  
QY 759 GAACTCTTCAGCCAGATTCTGAGGGCCAGCTATGAGTTTGACTCCCCCTTTTGGGATGAC 818  
Db 224 GluLeuPheSerGlnIleLeuArgAlaSerTyrGluPheAspSerProPheTrpAspAsp 243  
QY 819 ATCTCAGAAATCAGCCAAAGACTTCATTCCGCCACCTTCTGGAACGTGATCCCCAGAGAGG 878  
Db 244 IleSerGluSerAlaLysAspPheIleArgHisLeuLeuGluArgAspProGlnLysArg 263  
QY 879 TTCACCTGCCAGAGCCCTACAGCATCTTTGGATCTCTGGGGATGCAGCCCTTCGATAGG 938  
Db 264 PheThrCysGlnGlnAlaLeuArgHisLeuTrpIleSerGlyAspThrAlaPheAspArg 283  
QY 939 GACATCCTGGGTTCTGTGAGTGAGCAGATCCAGAAGAAATTTGCCAGGACCCACTGGAAG 998  
Db 284 AspIleLeuGlySerValSerGluGlnIleArgLysAsnPheAlaArgThrHisTrpLys 303

QY 999 CGTGCATTCAATGCCACATCATCTTCTACGTCCGTAGCTGGACAAAGCCCGAG 1058  
Db 304 ArgAlaPheAsnAlaThrSerPheLeuArgHisIleArgLysLeuGlyGlnIleProGlu 323  
QY 1059 GGTGAGGAGGCCCTCCAGGCGAGTGTATGACCCGTCATAGCCACCCAGGCCCTTGGGACTAGC 1118  
Db 324 GlyGluGlyAlaSerGluGlnGlyMetAlaArgHisSerHisSerGly----- 339  
QY 1119 CAGTCCCCCAAGTGGTGAAACCA-----GGTAGATGCCAAGGAAGGCCAAGT 1166  
Db 340 ---ProProCysTrpProAlaProGlnValMetProArgGlnMetProArgProSer 358  
QY 1167 GGACTGACTCCCGGTTTTTCTTTCTCCAGCCCTTTTGGTCTCTTCTCTGGATCCTTGTGTC 1226  
Db 359 GlyLeuThrProArgPheProSerLeuGlyCysPheArgSerProProProThrProPro 378  
QY 1227 CTCCAGACTGGCCTCTGCTGGAAGTCTGTGAGACTG---GGTGTGATGCATGGCACTAGGG 1283  
Db 379 ProGlyAlaGlyLeuCysTrp--IleLeuArgPheGluGlyValAlaHisGlyAlaGlyV 398  
QY 1284 TA---CGGGGCTTCCCCAGTATGTCCCCCAGCCTCTATTCTTACCTATGGTGGAGGCTCC 1340  
Db 398 alGlyMetGlyHisProGlnValCysProGlnAlaLeuProCysLeuGlyAlaValAlaP 418  
QY 1341 CTTTCCCATGT-----CGGTGCCACCCCTCTA-----TGGG 1370  
Db 418 roLeuProCysCysLeuSerArgProCysProProArgProAlaLysSerArgGlyGlyA 438  
QY 1371 AACTGAGGAGGTGTTCAAAAGTGGACTTGGGAGCCATCCTTCTCGCACCTTGCACGAACA 1430  
Db 438 laGlyArgArgAlaSer-----GlyAlaValPheProAlaArg----- 450  
QY 1431 CATGCATTGTGGCTGTTCTGTGCTTTGCTGACTGTGGTGGTCTGCTTGTGTGTGG 1490  
Db 451 -----LeuLeuCysAlaSerLeuSerValGlyGlyProAlaCysValMetV 466  
QY 1491 CCCTTTAGTTC 1501  
Db 466 alMetAlaPhe 469  
RESULT 2  
US-09-769-970-5  
; Sequence 5, Application US/09769970  
; Publication No. US20030170219A1  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; Hillman, Jennifer L.  
; Corley, Neil C.  
; Guegler, Karl G.  
; Lal, Preeti  
; Goli, Surya K.  
; Shah, Purvi  
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN  
; KINASES  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/769,970  
; FILING DATE: 24-Jan-2001  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/272,796  
;

; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J J  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0321 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; TELEX: <Unknown>  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 343 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: PROSNOT06  
; CLONE: 827431  
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:  
US-09-769-970-5

Alignment Scores:  
Pred. No.: 9.13e-121 Length: 343  
Score: 1625.00 Matches: 316  
Percent Similarity: 93.29% Conservatve: 4  
Best Local Similarity: 92.13% Mismatches: 23  
Query Match: 56.58% Indels: 0  
DB: 10 Gaps: 0

US-10-032-254A-1 (1-1554) x US-09-769-970-5 (1-343)

QY	105	ATGCTGCTGCTCAAGAAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAAG	164
Db	1	MetLeuLeuLeuLysHisThrGluAspIleSerSerValTyrGluIleArgGluArg	20
QY	165	CTGGGCTCGGGTGCCTTCTCTGAGGTGATGCTGGCCAGGAAAGGGCTCTGCTCATCTT	224
Db	21	LeuGlySerGlyAlaPheSerGluValValLeuAlaGlnGluArgGlySerAlaHisLeu	40
QY	225	GTGGCCCTCAAGTGCATTCCCAAGAACACTTCGGGGCAAGGAGGCCCTGGTGGAGAAT	284
Db	41	ValAlaLeuLysCysIleProLysLysAlaLeuArgGlyLysGluAlaLeuValGluAsn	60
QY	285	GAGATCGCGGTACTTCGCAGAATCAGCCATCCCAACATTGTGGCTCTGGAGCAGTCCAT	344
Db	61	GluIleAlaValLeuArgArgIleSerHisProAsnIleValAlaLeuGluAspValHis	80
QY	345	GAGAGTCCTTCTCTACTTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAAGTGTGAC	404
Db	81	GluSerProSerHisLeuTyrLeuAlaMetGluLeuValThrGlyGlyGluLeuPheAsp	100
QY	405	CGCATCATGGAGCGGGCTCCTACACAGAGAGGACGCCAGCCACCTTGTAGGGCAGGTC	464
Db	101	ArgIleMetGluArgGlySerTyrThrGluLysAspAlaSerHisLeuValGlyGlnVal	120
QY	465	CTTGGCGCTGTCTCTACCTTTCATAGCCTGGGCATCGTGCACCGGGACCTCAAGCCTGAA	524
Db	121	LeuGlyAlaValSerTyrLeuHisSerLeuGlyIleValHisArgAspLeuLysProGlu	140
QY	525	AACCTCCTCTATGCCACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTGGCCTG	584
Db	141	AsnLeuLeuTyrAlaThrProPheGluAspSerLysIleMetValSerAspPheGlyLeu	160
QY	585	TCCAAAATACAAGCTGGCAACATGCTAGGCACAGCTGTGGACCCCGATGTGGCC	644
Db	161	SerLysIleGlnAlaGlyAsnMetLeuGlyThrAlaCysGlyThrProGlyTyrValAla	180
QY	645	CCAGAGCTCCTGGAGCAGAAACCCCTACGGGAAGCGGTAGATGTGGGCCCTGGGTGC	704
Db	181	ProGluLeuLeuGluGlnLysProTyrGlyLysAlaValAspValTyrAlaLeuGlyVal	200
QY	705	ATCTCCTACATCCTGTGTGGGTACCCCTTCTATGATGAGAGCGGATCCTGAATC	764

Db	201	IleSerTyrIleLeuLeuCysGlyTyrProPheTyrAspGluSerAspProGluLeu	220
QY	765	TTCAGCCAGATTCTGAGGGCCAGCTATGAGTTTGACTCCCCCTTTTGGGATGACATCTCA	824
Db	221	PheSerGlnIleLeuArgAlaSerTyrGluPheAsp**ProPheTrpAspIleSer	240
QY	825	GAATCAGCCAAAGACTTCATTCCGCCACCTTCTGGAACGTATCCCCAGAGAGGTTCCAC	884
Db	241	GluSerGlyLysAspPheIleArgHisLeuLeuGluArgAspLeuGlnLysArgPheThr	260
QY	885	TGCCAGCAGGCCCTACAGCATCTTTGGATCTCTGGGGATGCAGCCTTCGATAGGGACATC	944
Db	261	CysGlnGlnAlaLeuArgAspLeuTrpIlePheTrpAspThrGlyPheGlyArgAspIle	280
QY	945	CTGGGTTCTGTCAGTGAGCAGATCCAGAAAGATTTTCCAGGACCCACTGGGAAGCGTGCA	1004
Db	281	LeuGlyPheValSerGluGlnIleArgLysAsnPheAlaTrpThrHisTrpLysArgAla	300
QY	1005	TTCAATGCCACATCATTCCTACGTCACATCCGTAAGCTGGGACAAAGCCAGAGGTTGAG	1064
Db	301	PheAsnAlaThrLeuPheLeuArgHisIleArgLysLeuGlyGlnIleProGluGlyGlu	320
QY	1065	GAGGCCTCCAGGCAGTGTATGACCCGTCATAGCCACCCAGGCCTTGGGACTAGCCAGTCC	1124
Db	321	GlyAlaSerGluGlnGlyMet**ArgHisSerHis**GlyLeuArgAlaGlyGlnPro	340
QY	1125	CCCAAGTGG 1133	
Db	341	ProLysTrp 343	

RESULT 3  
US-10-948-518-89  
; Sequence 89, Application US/10948518  
; Publication No. US20050064492A1  
; GENERAL INFORMATION:  
; APPLICANT: FREDERIC J. DESAUVAGE  
; APPLICANT: GRETCHEN FRANTZ  
; APPLICANT: KENNETH J. HILLAN  
; APPLICANT: PAUL POLAKIS  
; APPLICANT: ANDREW POLSON  
; APPLICANT: VICTORIA SMITH  
; APPLICANT: SUSAN D. SPENCER  
; APPLICANT: THOMAS D. WU  
; APPLICANT: ZEMIN ZHANG  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND  
; TITLE OF INVENTION: TREATMENT OF TUMOR  
; FILE REFERENCE: P5026R1-US  
; CURRENT APPLICATION NUMBER: US/10/948,518  
; CURRENT FILING DATE: 2004-09-22  
; PRIOR APPLICATION NUMBER: US/10/643,795  
; PRIOR FILING DATE: 2003-08-19  
; PRIOR APPLICATION NUMBER: US 60/404,809  
; PRIOR FILING DATE: 2002-08-19  
; PRIOR APPLICATION NUMBER: US 60/405,645  
; PRIOR FILING DATE: 2002-08-21  
; PRIOR APPLICATION NUMBER: US 60/413,192  
; PRIOR FILING DATE: 2002-09-23  
; PRIOR APPLICATION NUMBER: US 60/419,008  
; PRIOR FILING DATE: 2002-10-15  
; PRIOR APPLICATION NUMBER: US 60/426,847  
; PRIOR FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/484,959  
; PRIOR FILING DATE: 2003-07-02  
; NUMBER OF SEQ ID NOS: 158  
; SEQ ID NO 89  
; LENGTH: 343  
; TYPE: PRP  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: Unsure  
; LOCATION: 233, 328, 333  
; OTHER INFORMATION: Unknown amino acid  
US-10-948-518-89

Alignment Scores:  
Pred. No.: 9.13e-121 Length: 343  
Score: 1625.00 Matches: 316  
Percent Similarity: 93.29% Conservative: 4  
Best Local Similarity: 92.13% Mismatches: 23  
Query Match: 56.58% Indels: 0  
DB: 17 Gaps: 0

US-10-032-254A-1 (1-1554) x US-10-948-518-89 (1-343)

QY 105 ATGCTGCTGCTCAAGAAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAAG 164  
Db 1 MetLeuLeuLeuLysHisThrGluAspLleSerSerValTyrGluIleArgGluArg 20  
QY 165 CTGGGCTCGGTGCTCTCTGAGGTGATGCTGGCCCCAGGAAAGGGCTCTGCTCATCTT 224  
Db 21 LeuGlySerGlyAlaPheSerGluValValIleuAlaGlnGluArgGlySerAlaHisLeu 40  
QY 225 GTGGCCCTCAAGTGCATTCCTCCAGAAAGCACTTCGGGGCAAGGAGGCCCTGGTGAGAAT 284  
Db 41 ValAlaLeuLysCysIleProLysLysAlaLeuArgGlyLysGluAlaLeuValGluAsn 60  
QY 285 GAGATCGCGGTACTTCGAGAAATCAGCCATCCCAACATTGTGGCTCTGGAGGACGTCCAT 344  
Db 61 GluIleAlaValLeuArgArgIleSerHisProAsnIleValAlaLeuGluAspValHis 80  
QY 345 GAGATCCTTCTCATCTCTACTTGGCCATGGAGCTGGTAACAGGTGTGAACCTGTTTGAC 404  
Db 81 GluSerProSerHisLeuTyrLeuAlaMetGluLeuValThrGlyGlyGluLeuPheAsp 100  
QY 405 CGCATCATGGAGGGGCTCCTACACAGAGAAGACGCCAGCCACCTTGTAGGGCAGGTC 464  
Db 101 ArgIleMetGluArgGlySerTyrThrGluLysAspAlaSerHisLeuValGlyGlnVal 120  
QY 465 CTTGGCGCTGTCTCTACCTTCATAGCCTGGGCATCGTGCACCGGACCTCAAGCCTGAA 524  
Db 121 LeuGlyAlaValSerTyrLeuHisSerLeuGlyIleValHisArgAspLeuLysProGlu 140  
QY 525 AACCTCCTCTATGCCACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTGGCCTG 584  
Db 141 AsnLeuLeuTyrAlaThrPropheGluAspSerLysIleMetValSerAspPheGlyLeu 160  
QY 585 TCCAAAATACAAGCTTGGCAACATGCTAGGCACAGCCTGTGGGACCCCGAGATATGTGCC 644  
Db 161 SerLysIleGlnAlaGlyAsnMetLeuGlyThrAlaCysGlyThrProGlyTyrValAla 180  
QY 645 CCAGAGCTCCTGGAGCAGAAACCCCTACGGGAAGCCGTAGATGTGTGGGCCCTGGGTGC 704  
Db 181 ProGluLeuLeuGluGlnLysProTyrGlyLysAlaValAspValTrpAlaLeuGlyVal 200  
QY 705 ATCTCTACATCCTGTGTGGTACCCCTCTCTATGATGAGAGCGATCCTGAACTC 764  
Db 201 IleSerTyrIleLeuLeuCysGlyTyrProProPheTyrAspGluSerAspProGluLeu 220  
QY 765 TTCAGCCAGATTCTGAGGGCCAGCTATGAGTTTGACTCCCTCTTGGGATGACATCTCA 824  
Db 221 PheSerGlnIleLeuArgAlaSerTyrGluPheAsp\*\*PropheTrpAspAspIleSer 240  
QY 825 GAATCAGCCAAAGACTTCATTGCCCACCTTCTGGRAAGTGTATCCCCAGAGAGGTTTACC 884  
Db 241 GluSerGlyLysAspPheIleArgHisLeuLeuGluArgAspLeuGlnLysArgPheThr 260  
QY 885 TGCCAGCAGGCCCTACAGCATCTTTGGATCTCTGGGATGCAGCCTTCGATAGGGACATC 944  
Db 261 CysGlnGlnAlaLeuArgAspLeuTrpIlePheTrpAspThrGlyPheGlyArgAspIle 280  
QY 945 CTGGGTTCTGTAGTGAGCAGATCCAGAAGAAATTTGCCAGGACCCACTGGAGCGGTGCA 1004  
Db 281 LeuGlyPheValSerGluGlnIleArgLysAsnPheAlaTrpThrHisTrpLysArgAla 300  
QY 1005 TTCAATGCCACATCATTCCTACGTCACATCCGTAAGCTGGGACAAAGCCCGAGGGGTGAG 1064

Db 301 PheAsnAlaThrLeuPheLeuArgHisIleArgLysLeuGlyGlnIleProGluGlyGlu 320  
QY 1065 GAGGCCTCCAGGCAGTGTATGACCCGTATAGCCACCCAGGCTTGGGACTAGCCAGTCC 1124  
Db 321 GlyAlaSerGluGlnGlyMet\*\*\*ArgHisSerHis\*\*\*GlyLeuArgAlaGlyGlnPro 340  
QY 1125 CCCAAGTGG 1133  
Db 341 ProLysTrp 343  
RESULT 4  
US-10-664-421-13  
; Sequence 13, Application US/10664421  
; Publication No. US20040142864A1  
; GENERAL INFORMATION:  
; APPLICANT: BREMER, RYAN  
; APPLICANT: IBRAHIM, PRABHA  
; APPLICANT: KUMAR, ABHINAV  
; APPLICANT: MANDIYAN, VALSAN  
; APPLICANT: MILBURN, MICHAEL V.  
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE  
; FILE REFERENCE: 039363/0703  
; CURRENT APPLICATION NUMBER: US/10/664,421  
; CURRENT FILING DATE: 2003-09-16  
; PRIOR APPLICATION NUMBER: 60/412,341  
; PRIOR FILING DATE: 2002-09-20  
; PRIOR APPLICATION NUMBER: 60/411,398  
; PRIOR FILING DATE: 2002-09-16  
; NUMBER OF SEQ ID NOS: 169  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 13  
; LENGTH: 332  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-664-421-13  
Alignment Scores:  
Pred. No.: 1.28e-85 Length: 332  
Score: 1184.50 Matches: 220  
Percent Similarity: 85.17% Conservative: 50  
Best Local Similarity: 69.40% Mismatches: 44  
Query Match: 41.24% Indels: 3  
DB: 16 Gaps: 2  
US-10-032-254A-1 (1-1554) x US-10-664-421-13 (1-332)  
QY 120 AAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGGAGAAAGTGGGCTCGGTGCC 179  
Db 11 LysGlnAlaGluAspIleArgAspIleTyrAspPheArgAspValLeuGlyThrGlyAla 30  
QY 180 TTCTCTGAGGTGATGCTGGCCAGGAAAGGGCTCTGCTCATCTTGTGGCCCTCAAGTGC 239  
Db 31 PheSerGluValIleLeuAlaGluAspLysArgThrGlnLysLeuValAlaIleLysCys 50  
QY 240 ATTCCCAAGAAAGCACTTCGGGGCAAGGAGGCCCTGGTGGAGAAATGAGATCGCGGTACTT 299  
Db 51 IleAlaLysLysAlaLeuGluGlyLysGluGlySerMetGluAsnGluIleAlaValLeu 70  
QY 300 CGCAGAATCAGCCATCCCAACATTGTGGTCTTGGAGGACGTCCATGAGAGTCTTCTCAT 359  
Db 71 HisLysIleLysHisProAsnIleValAlaLeuAspAspIleTyrGluSerGlyGlyHis 90  
QY 360 CTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAACCTGTTTGACCGCATCATGGAGCGG 419  
Db 91 LeuTyrLeuIleMetGlnLeuValSerGlyGlyGluLeuPheAspArgIleValGluLys 110  
QY 420 GGCTCCTACACAGAGAAGGACGCCAGCCACTTGTAGGGCAGGTCTTGGCGCTGTCTCC 479  
Db 111 GlyPheTyrThrGluArgAspAlaSerArgLeuIlePheGlnValLeuAspAlaValLys 130  
QY 480 TACCTTCATAGCTGGGCATCGTGCACCGGACCTCAAGCCTGAAAAACCTCTCTATGCC 539  
Db 131 TyrLeuHisAspLeuGlyIleValHisArgAspLeuLysProGluAsnLeuLeuTyrTyr 150



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QY 540 ACACCTTTTGAGGACTCCAGATCATGGTCTCTGACTTTGGCCTGTCCAAAATACAA--- 596
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Db 151 SerLeuAspGluAspSerLysIleMetIleSerAspPheGlyLeuSerLysMetGluAsp 170
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QY 597 GCTGGCAACATGCTAGGCACAGCCTGTGGACCCCGAGATATGTGGCCCGCAGAGCTCCTG 656
   |||::: ||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 171 ProGlySerValLeuSerThrAlaCysGlyThrProGlyTyrValAlaProGluValLeu 190
   |||::: ||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 657 GAGCAGAAACCTACGGGAAGCCGCTAGATGTGTGGGCCCTGGGTGTCATCTCCTACATC 716
   ||||||| ||||||| ||||||| ||||||| |||::: ||| ||||||| ||||||| |||||||
Db 191 AlaGlnLysProTyrSerLysAlaValAspCysTrpSerIleGlyValIleAlaTyrIle 210
   |||::: ||| ||||||| ||||||| ||||||| ||||||| |||::: ||| ||||||| |||||||
QY 717 CTGCTGTGGGTACCCCCCTTCTATGATGAGAGCGATCCTGAACTCTTCAGCCAGATT 776
   ||||||| ||||||| ||||||| ||||||| |||::: ||| ||||||| ||||||| |||||||
Db 211 LeuLeuCysGlyTyrProProPheTyrAspGluAsnAspAlaLysLeuPheGluGlnIle 230
   |||::: ||| ||||||| ||||||| ||||||| |||::: ||| ||||||| ||||||| |||||||
QY 777 CTGAGGGCCAGCTATGAGTTTGACTCCCCCTTTTGGGATGACATCTCAGAAATCAGCCAAA 836
   |||::: ||| ||||||| ||||||| |||::: ||| ||||||| ||||||| |||||||
Db 231 LeuLysAlaGluTyrGluPheAspSerProTyrTrpAspAspIleSerAspSerAlaLys 250
   |||::: ||| ||||||| ||||||| |||::: ||| ||||||| ||||||| |||||||
QY 837 GACTTCATTGCGCACCTTCTGGAACGTGATCCCCAGAGAGGTTACCTGCCAGGAGCC 896
   ||||||| ||||||| |||::: ||| ||||||| |||::: ||| ||||||| ||||||| |||||||
Db 251 AspPheIleArgHisLeuMetGluLysAspProGluLysArgPheThrCysGluGlnAla 270
   |||::: ||| ||||||| ||||||| |||::: ||| ||||||| ||||||| |||||||
QY 897 CTACAGCATCTTTGGATCTCTGGGGATGCAGCCTTCGATAGGGACATCCTGGGTTCTGTC 956
   ||||||| ||||||| |||::: ||| ||||||| |||::: ||| ||||||| ||||||| |||||||
Db 271 LeuGlnHisProTrpIleAlaGlyAspThrAlaLeuAspLysAsnIleHisGlnSerVal 290
   |||::: ||| ||||||| ||||||| |||::: ||| ||||||| ||||||| |||||||
QY 957 AGTGAGCAGATCCAGAAAGATTTTGGCAGGACCCACTGGAAGCGTGCATTCAATGCCACA 1016
   ||||||| |||::: ||| ||||||| |||::: ||| ||||||| ||||||| |||||||
Db 291 SerGluGlnIleLysLysAsnPheAlaLysSerLysTrpLysGlnAlaPheAsnAlaThr 310
   |||::: ||| ||||||| ||||||| |||::: ||| ||||||| ||||||| |||||||
QY 1017 TCATTCTACGTACATCCGTAAG-----CTGGGACAAAGCCCGAGGGGT 1061
   ::: |||::: ||| ||||||| ||||||| ||| ||| |||
Db 311 AlaValValArgHisMetArgLysLeuGlnLeuGlyHisGlnProGlyGly 327

RESULT 5
US-09-817-181-4
; Sequence 4, Application US/09817181
; Patent No. US20020142427A1
; GENERAL INFORMATION:
; APPLICANT: MERKULOV, Gennady et al
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001189
; CURRENT APPLICATION NUMBER: US/09/817,181
; CURRENT FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 370
; TYPE: PRT
; ORGANISM: Human
US-09-817-181-4

Alignment Scores:
Pred. No.: 1.32e-85 Length: 370
Score: 1184.50 Matches: 220
Percent Similarity: 85.53% Conservative: 52
Best Local Similarity: 69.18% Mismatches: 43
Query Match: 41.24% Indels: 3
DB: 9 Gaps: 2

US-10-032-254A-1 (1-1554) x US-09-817-181-4 (1-370)

QY 120 AAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAGCTGGGCTCGGTGCC 179
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Db 11 LysGlnAlaGluAspIleArgAspIleTyrAspPheArgAspValLeuGlyThrGlyAla 30
   |||::: ||| ||||||| ||||||| |||::: ||| ||||||| ||||||| |||||||
QY 180 TTCTCTGAGGTGATCTGGCCAGGAAAGGGCTCTGCTCATCTTGTGGCCCTCAAGTGC 239
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Db 31 PheSerGluValIleLeuAlaGluAspLysArgThrGlnLysLeuValAlaIleLysCys 50
QY 240 ATTCCTCAAGAAAGCACTTCGGGGCAAGGAGGCCCTGCTGGAGAATGAGATCGCGTACTT 299
   ||| |||::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 51 IleAlaLysGluAlaLeuGluGlyLysGluGlySerMetGluAsnGluIleAlaValLeu 70
QY 300 CGCAGAATCAGCCATCCCAACATTGTGGCTCTGAGAGACGTCCATGAGAGTCTCTCTCAT 359
   ::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 71 HisLysIleLysHisProAsnIleValAlaLeuAspAspIleTyrGluSerGlyGlyHis 90
QY 360 CTCTACTTTGGCCATGAGACTGGTAACAGGTGGTGAACCTGTTGACCGCATCATGGAGCGG 419
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 91 LeuTyrLeuIleMetGlnLeuValSerGlyGlyGluLeuPheAspArgIleValGluLys 110
QY 420 GGCTCCTACACAGAGAAGGACGCCAGCCACCTTGTAGGGCAGGTCTTGGCGCTGTCTCC 479
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 111 GlyPheTyrThrGluArgAspAlaSerArgLeuIlePheGlnValLeuAspAlaValLys 130
QY 480 TACCTTCATAGCTGGGCATCGTGCACCGGGACCTCAAGCCTGAAAAACCTCTCTATGCC 539
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 131 TyrLeuHisAspLeuGlyIleValHisArgAspLeuLysProGluAsnLeuLeuTyrTyr 150
QY 540 ACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTGGCCTGTCCAAAATACAA--- 596
   ::: ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 151 SerLeuAspGluAspSerLysIleMetIleSerAspPheGlyLeuSerLysMetGluAsp 170
QY 597 GCTGGCAACATGCTAGGCACAGCCTGTGGACCCCGAGATATGTGGCCCGCAGAGCTCCTG 656
   |||::: ||| ||||||| ||||||| ||||||| ||||||| |||::: ||| ||||||| |||||||
Db 171 ProGlySerValLeuSerThrAlaCysGlyThrProGlyTyrValAlaProGluValLeu 190
QY 657 GAGCAGAAACCTTACGGGAAGCCGCTAGATGTGTGGGCCCTGGGTGTCATCTCCTACATC 716
   ||||||| ||||||| |||::: ||| ||||||| |||::: ||| ||||||| ||||||| |||||||
Db 191 AlaGlnLysProTyrSerLysAlaValAspCysTrpSerIleGlyValIleAlaTyrIle 210
QY 717 CTGCTGTGGGTACCCCCCTTCTATGATGAGAGCGATCCTGAACTCTTCAGCCAGATT 776
   ||||||| ||||||| ||||||| ||||||| |||::: ||| ||||||| ||||||| |||||||
Db 211 LeuLeuCysGlyTyrProProPheTyrAspGluAsnAspAlaLysLeuPheGluGlnIle 230
QY 777 CTGAGGGCCAGCTATGAGTTTGACTCCCCCTTTTGGGATGACATCTCAGAAATCAGCCAAA 836
   |||::: ||| ||||||| ||||||| |||::: ||| ||||||| ||||||| |||||||
Db 231 LeuLysAlaGluTyrGluPheAspSerProTyrTrpAspAspIleSerAspSerAlaLys 250
QY 837 GACTTCATTGCGCACCTTCTGGAACGTGATCCCCAGAGAGGTTACCTGCCAGGAGCC 896
   ||||||| ||||||| |||::: ||| ||||||| |||::: ||| ||||||| ||||||| |||||||
Db 251 AspPheIleArgHisLeuMetGluLysAspProGluLysArgPheThrCysGluGlnAla 270
QY 897 CTACAGCATCTTTGGATCTCTGGGGATGCAGCCTTCGATAGGGACATCCTGGGTTCTGTC 956
   ||||||| ||||||| |||::: ||| ||||||| |||::: ||| ||||||| ||||||| |||||||
Db 271 LeuGlnHisProTrpIleAlaGlyAspThrAlaLeuAspLysAsnIleHisGlnSerVal 290
QY 957 AGTGAGCAGATCCAGAAAGATTTTGGCAGGACCCACTGGAAGCGTGCATTCAATGCCACA 1016
   ||||||| |||::: ||| ||||||| |||::: ||| ||||||| ||||||| |||||||
Db 291 SerGluGlnIleLysLysAsnPheAlaLysSerLysTrpLysGlnAlaPheAsnAlaThr 310
QY 1017 TCATTCTACGTACATCCGTAAG-----CTGGGACAAAGCCCGAGGGTGAG 1064
   ::: |||::: ||| ||||||| ||||||| ||| ||| |||
Db 311 AlaValValArgHisMetArgLysLeuGlnLeuGlyThrSerGlnGluGlyGln 328

RESULT 6
US-09-769-970-19
; Sequence 19, Application US/09769970
; Publication No. US20030170219A1
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; Hillman, Jennifer L.
; Corley, Neil C.
; Guegler, Karl G.
; Lal, Preeti
; Goli, Surya K.
; Shah, Purvi
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN
; KINASES
; NUMBER OF SEQUENCES: 21
```

;;  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
;; STREET: 3174 Porter Drive  
;; CITY: Palo Alto  
;; STATE: CA  
;; COUNTRY: USA  
;; ZIP: 94304  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Diskette  
;; COMPUTER: IBM Compatible  
;; OPERATING SYSTEM: DOS  
;; SOFTWARE: FastSEQ for Windows Version 2.0  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/769,970  
;; FILING DATE: 24-Jan-2001  
;; CLASSIFICATION: <Unknown>  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 09/272,796  
;; FILING DATE: <Unknown>  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Billings, Lucy J J  
;; REGISTRATION NUMBER: 36,749  
;; REFERENCE/DOCKET NUMBER: PF-0321 US  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 415-855-0555  
;; TELEFAX: 415-845-4166  
;; TELEX: <Unknown>  
;; INFORMATION FOR SEQ ID NO: 19:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 370 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; IMMEDIATE SOURCE:  
;; LIBRARY: GenBank  
;; CLONE: 790790  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 19:  
US-09-769-970-19

Alignment Scores:  
Pred. No.: 1.32e-85 Length: 370  
Score: 1184.50 Matches: 220  
Percent Similarity: 85.53% Conservative: 52  
Best Local Similarity: 69.18% Mismatches: 43  
Query Match: 41.24% Indels: 3  
DB: 10 Gaps: 2

US-10-032-254A-1 (1-1554) x US-09-769-970-19 (1-370)

QY 120 AAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAGCTGGGTCGGGTGCC 179  
Db 11 LysGlnAlaGluAspIleTyrArgAspIleTyrAspPheArgAspValLeuGlyThrGlyAla 30  
QY 180 TTCTCTGAGGTGATGCTGGCCCCAGGAAAGGGCTCTGCTCATCTTGTGGCCCTCAAGTGC 239  
Db 31 PheSerGluValIleLeuAlaGluAspLysArgThrGlnLysLeuValAlaIleLysCys 50  
QY 240 ATTCCCAAGAAAGCACTTCGGGGCAAGGAGGCCCTGCTGGAGAGATGAGATCGCGGTACTT 299  
Db 51 IleAlaLysGluAlaLeuGluGlyLysGluGlySerMetGluAsnGluIleAlaValLeu 70  
QY 300 CGCAGAATCAGCCATCCCAACATTGTGGCTCTGGAGGACGTCCATGAGAGTCTTCTCAT 359  
Db 71 HisLysIleLysHisProAsnIleValAlaLeuAspAspIleTyrGluSerGlyGlyHis 90  
QY 360 CTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAAGTGGTGAAGTGGTGAAGTGGTGAAG 419  
Db 91 LeuTyrLeuIleMetGlnLeuValSerGlyGlyGluPheAspArgIleValGluLys 110  
QY 420 GGCTCCTACACAGAGAGAGAGCCAGCCACCTTGTAGGGCAGGTCTCTGGCGTGTCTCC 479  
Db 111 GlyPheTyrThrGluArgAspAlaSerArgLeuIlePheGlnValLeuAspAlaValLys 130

QY 480 TACCTTCATAGCCTGGGCATCGTGACCGGACCTCAAGCCTGAAAAACCTCCTCTATGCC 539  
Db 131 TyrLeuHisAspLeuGlyIleValHisArgAspLeuLysProGluAenLeuLeuTyrTyr 150  
QY 540 ACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTTGGCCTGTCCAAAAATACAA --- 596  
Db 151 SerLeuAspGluAspSerLysIleMetIleSerAspPheGlyLeuSerLysMetGluAsp 170  
QY 597 GCTGGCAACATGCTAGGCACAGCCTGTGGACCCCGAGGATATGTGGCCCCAGAGCTCCTG 656  
Db 171 ProGlySerValLeuSerThrAlaCysGlyThrProGlyTyrValAlaProGluValLeu 190  
QY 657 GAGCAGAAACCCTACGGGAAGCCGTAGATGTGTGGCCCTGGGTGTCATCTCCTACATC 716  
Db 191 AlaGlnLysProTyrSerLysAlaValAspCysTrpSerIleGlyValIleAlaTyrIle 210  
QY 717 CTGCTGTGTGGGTACCCCCCTTCTATGATGAGAGCGATCCTGAACCTCTTCAGCCAGATT 776  
Db 211 LeuLeuCysGlyTyrProProPheTyrAspGluAsnAspAlaLysLeuPheGluGlnIle 230  
QY 777 CTGAGGSCCAGCTATGAGTTTGACTCCCTCTTTGGGATGACATCTCAGAAATCAGCCAAA 836  
Db 231 LeuLysAlaGluTyrGluPheAspSerProTyrTrpAspAspIleSerAspSerAlaLys 250  
QY 837 GACTTCATTCGCCACCTTCTGGAACGTGATCCCCCAGAGAGGTTTCACCTGCCAGCGCC 896  
Db 251 AspPheIleArgHisLeuMetGluLysAspProGluLysArgPheThrCysGluGlnAla 270  
QY 897 CTACAGCATCTTTGGATCTCTGGGGATGCAGCCCTTCGATAGGGACATCCTGGGTCTGTC 956  
Db 271 LeuGlnHisProTrpIleAlaGlyAspThrAlaLeuAspLysAsnIleHisGlnSerVal 290  
QY 957 AGTGAGCAGATCCAGAAGATTTTGCCAGGACCCACTGGAAGCGTGCAATCAATGCCACA 1016  
Db 291 SerGluGlnIleLysLysAsnPheAlaLysSerLysTrpLysGlnAlaPheAsnAlaThr 310  
QY 1017 TCATTCTACGTACATCCCGTAAG-----CTGGACAAAGCCCCAGAGGTTGAG 1064  
Db 311 AlaValValArgHisMetArgLysLeuGlnLeuGlyThrSerGlnGluGlyGln 328

RESULT 7  
US-10-142-356-7  
; Sequence 7, Application US/10142356  
; Publication No. US20030036183A1  
; GENERAL INFORMATION:  
; APPLICANT: Boylan, John F.  
; APPLICANT: Bowers, Alex J.  
; TITLE OF INVENTION: Serine-Threonine Kinase Member, h2520-40  
; FILE REFERENCE: 01017/37177A  
; CURRENT APPLICATION NUMBER: US/10/142,356  
; CURRENT FILING DATE: 2002-05-09  
; PRIOR APPLICATION NUMBER: 60/290,276  
; PRIOR FILING DATE: 2001-05-10  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 7  
; LENGTH: 370  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-142-356-7

Alignment Scores:  
Pred. No.: 1.32e-85 Length: 370  
Score: 1184.50 Matches: 220  
Percent Similarity: 85.53% Conservative: 52  
Best Local Similarity: 69.18% Mismatches: 43  
Query Match: 41.24% Indels: 3  
DB: 14 Gaps: 2

US-10-032-254A-1 (1-1554) x US-10-142-356-7 (1-370)

QY 120 AAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAGCTGGGTCGGGTGCC 179  
Db 111 GlyPheTyrThrGluArgAspAlaSerArgLeuIlePheGlnValLeuAspAlaValLys 130

Db 11 LysGlnAlaGluAspIleArgAspIleTyrAspPheArgAspValLeuGlyThrGlyAla 30  
QY 180 TTCTCTGAGGTGATGCTGGCCAGGAAAGGGCTCTGCTCATCTTGTGGCCCTCAAGTGC 239  
Db 31 PheSerGluValIleLeuAlaGluAspLysArgThrGlnLysLeuValAlaIleLysCys 50  
QY 240 ATTCCCAAGAAAGCACTTCGGGGCAAGGAGGCCCTGGTGAGAAATGAGATCGCGGTACTT 299  
Db 51 IleAlaLysGluAlaLeuGluGlyLysGluGlySerMetGluAsnGluIleAlaValLeu 70  
QY 300 CGCAGAATCAGCCATCCCAACATTGTGGCTCTGGAGGACGTCCATGAGAGTCCTTCTCAT 359  
Db 71 HisLysIleLysHisProAsnIleValAlaLeuAspAspIleTyrGluSerGlyGlyHis 90  
QY 360 CTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAACCTGTTGACCGCATCATGGAGCGG 419  
Db 91 LeuTyrLeuIleMetGlnLeuValSerGlyGlyGluLeuPheAspArgIleValGluLys 110  
QY 420 GGCTCCTACACAGAGAGGACGCCAGCCACCTTGTAGGGCAGGTCTCTGGCGCTGTCTCC 479  
Db 111 GlyPheTyrThrGluArgAspAlaSerArgLeuIlePheGlnValLeuAspAlaValLys 130  
QY 480 TACCTTCATAGCCTGGGCATCGTGCCACCGGACCTCAAGCCTGAAACCTCTCTATGCC 539  
Db 131 TyrLeuHisAspLeuGlyIleValHisArgAspLeuLysProGluAsnLeuLeuTyrTyr 150  
QY 540 ACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTGGCCTGTGCCAAATACAA--- 596  
Db 151 SerLeuAspGluAspSerLysIleMetIleSerAspPheGlyLeuSerLysMetGluAsp 170  
QY 597 GCTGGCAACATGCTAGGCACAGCCTGTGGGACCCAGGATATGTGGCCCGCAGAGCTCCTG 656  
Db 171 ProGlySerValLeuSerThrAlaCysGlyThrProGlyTyrValAlaProGluValLeu 190  
QY 657 GAGCAGAAACCTTACGGGAAGCGGTAGATGTGTGGCCCTGGGTGTCTCTCTACATC 716  
Db 191 AlaGlnLysProTyrSerLysAlaValAspCysTrpSerIleGlyValIleAlaTyrIle 210  
QY 717 CTGCTGTGGGTACCCCTTCTATGATGAGAGCGATCCTGAACTCTTCAGCCAGATT 776  
Db 211 LeuLeuCysGlyTyrProPheTyrAspGluAsnAspAlaLysLeuPheGluGlnIle 230  
QY 777 CTGAGGGCCAGCTATGAGTTTGACTCCCTTTTGGGATGACATCTCAGAAATCAGCCAAA 836  
Db 231 LeuLysAlaGluTyrGluPheAspSerProTyrTrpAspAspIleSerAspSerAlaLys 250  
QY 837 GACTTCATTGCCACCTTCTGGAACGTGATCCCGAGAGGTTTCACCTGCCAGCGCC 896  
Db 251 AspPheIleArgHisLeuMetGluLysAspProGluLysArgPheThrCysGluGlnAla 270  
QY 897 CTACAGCATCTTTGGATCTCTGGGGATGCAGCCTTCGATAGGGACATCCTGGTTCTGTC 956  
Db 271 LeuGlnHisProTrpIleAlaGlyAspThrAlaLeuAspLysAsnIleHisGlnSerVal 290  
QY 957 AGTGAGCAGATCCAGAAGAAATTTGCCAGGACCCACTGGAAGCGTGCATTCAATGCCACA 1016  
Db 291 SerGluGlnIleLysLysAsnPheAlaLysSerLysTrpLysGlnAlaPheAsnAlaThr 310  
QY 1017 TCATTCTACGTACATCCGTAAG-----CTGGACAAAGCCCGAGAGGTGAG 1064  
Db 311 AlaValValArgHisMetArgLysLeuGlnLeuGlyThrSerGlnGluGlyGln 328

RESULT 8

US-10-300-828-4  
; Sequence 4, Application US/10300828  
; Publication No. US2003007799A1  
; GENERAL INFORMATION:  
; APPLICANT: MERKULOV, Gennady et al  
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC  
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES  
; TITLE OF INVENTION: THEREOF  
; FILE REFERENCE: CL001189CON  
; CURRENT APPLICATION NUMBER: US/10/300,828

; CURRENT FILING DATE: 2002-11-21  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 370  
; TYPE: PRT  
; ORGANISM: Human  
US-10-300-828-4  
  
Alignment Scores:  
Pred. No.: 1.32e-85 Length: 370  
Score: 1184.50 Matches: 220  
Percent Similarity: 85.53% Conservative: 52  
Best Local Similarity: 69.18% Mismatches: 43  
Query Match: 41.24% Indels: 3  
DB: 14 Gaps: 2

US-10-032-254A-1 (1-1554) x US-10-300-828-4 (1-370)

QY 120 AAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAAAGCTGGGCTCGGGTGCC 179  
Db 11 LysGlnAlaGluAspIleArgAspIleTyrAspPheArgAspValLeuGlyThrGlyAla 30  
QY 180 TTCTCTGAGGTGATGCTGGCCAGGAAAGGGCTCTGCTCATCTTGTGGCCCTCAAGTGC 239  
Db 31 PheSerGluValIleLeuAlaGluAspLysArgThrGlnLysLeuValAlaIleLysCys 50  
QY 240 ATTCCCAAGAAAGCACTTCGGGGCAAGGAGGCCCTGGTGAGAAATGAGATCGCGGTACTT 299  
Db 51 IleAlaLysGluAlaLeuGluGlyLysGluGlySerMetGluAsnGluIleAlaValLeu 70  
QY 300 CGCAGAATCAGCCATCCCAACATTGTGGCTCTGGAGGACGTCCATGAGAGTCCTTCTCAT 359  
Db 71 HisLysIleLysHisProAsnIleValAlaLeuAspAspIleTyrGluSerGlyGlyHis 90  
QY 360 CTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAACCTGTTGACCGCATCATGGAGCGG 419  
Db 91 LeuTyrLeuIleMetGlnLeuValSerGlyGlyGluLeuPheAspArgIleValGluLys 110  
QY 420 GGCTCCTACACAGAGAGGACGCCAGCCACCTTGTAGGGCAGGTCTCTGGCGCTGTCTCC 479  
Db 111 GlyPheTyrThrGluArgAspAlaSerArgLeuIlePheGlnValLeuAspAlaValLys 130  
QY 480 TACCTTCATAGCCTGGGCATCGTGCCACCGGACCTCAAGCCTGAAACCTCTCTATGCC 539  
Db 131 TyrLeuHisAspLeuGlyIleValHisArgAspLeuLysProGluAsnLeuLeuTyrTyr 150  
QY 540 ACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTGGCCTGTCCAAAATACAA--- 596  
Db 151 SerLeuAspGluAspSerLysIleMetIleSerAspPheGlyLeuSerLysMetGluAsp 170  
QY 597 GCTGGCAACATGCTAGGCACAGCCTGTGGGACCCAGGATATGTGGCCCGCAGAGCTCCTG 656  
Db 171 ProGlySerValLeuSerThrAlaCysGlyThrProGlyTyrValAlaProGluValLeu 190  
QY 657 GAGCAGAAACCTTACGGGAAGCGGTAGATGTGTGGCCCTGGGTGTCTCATCTCTACATC 716  
Db 191 AlaGlnLysProTyrSerLysAlaValAspCysTrpSerIleGlyValIleAlaTyrIle 210  
QY 717 CTGCTGTGGGTACCCCTTCTATGATGAGAGCGATCCTGAACTCTTCAGCCAGATT 776  
Db 211 LeuLeuCysGlyTyrProPheTyrAspGluAsnAspAlaLysLeuPheGluGlnIle 230  
QY 777 CTGAGGGCCAGCTATGAGTTTGACTCCCTTTTGGGATGACATCTCAGAAATCAGCCAAA 836  
Db 231 LeuLysAlaGluTyrGluPheAspSerProTyrTrpAspAspIleSerAspSerAlaLys 250  
QY 837 GACTTCATTGCCACCTTCTGGAACGTGATCCCGAGAGGTTTCACCTGCCAGCGCC 896  
Db 251 AspPheIleArgHisLeuMetGluLysAspProGluLysArgPheThrCysGluGlnAla 270  
QY 897 CTACAGCATCTTTGGATCTCTGGGGATGCAGCCTTCGATAGGGACATCCTGGTTCTGTC 956  
Db 271 LeuGlnHisProTrpIleAlaGlyAspThrAlaLeuAspLysAsnIleHisGlnSerVal 290  
QY 957 AGTGAGCAGATCCAGAAGAAATTTGCCAGGACCCACTGGAAGCGTGCATTCAATGCCACA 1016  
Db 291 SerGluGlnIleLysLysAsnPheAlaLysSerLysTrpLysGlnAlaPheAsnAlaThr 310  
QY 1017 TCATTCTACGTACATCCGTAAG-----CTGGACAAAGCCCGAGAGGTGAG 1064  
Db 311 AlaValValArgHisMetArgLysLeuGlnLeuGlyThrSerGlnGluGlyGln 328



Db 271 LeuGlnHisProTrpIleAlaGlyAspThrAlaLeuAspLysAsnIleHisGlnSerVal 290

QY 957 AGTGAGCATCCAGAAGAATTTTGGCAGGACCCACTGGAAGCGTGCATTCAATGCCACA 1016

Db 291 SerGluGlnIleLysLysAsnPheAlaLysSerLysTrpLysGlnAlaPheAsnAlaThr 310

QY 1017 TCATTCTACGTACATCCGTAAG-----CTGGGACAAAGCCCGAGGGTGAG 1064

Db 311 AlaValValArgHisMetArgLysLeuGlnLeuGlyThrSerGlnGluGlyGln 328

RESULT 9

US-10-090-002-4

; Sequence 4, Application US/10090002

; Publication No. US20030175926A1

; GENERAL INFORMATION:

; APPLICANT: YAN, Chunhua et al.

; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: CL001316

; CURRENT APPLICATION NUMBER: US/10/090,002

; CURRENT FILING DATE: 2002-03-08

; NUMBER OF SEQ ID NOS: 4

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 370

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-090-002-4

Alignment Scores:

Pred. No.:	1.32e-85	Length:	370
Score:	1184.50	Matches:	220
Percent Similarity:	85.53%	Conservative:	52
Best Local Similarity:	69.18%	Mismatches:	43
Query Match:	41.24%	Indels:	3
DB:	14	Gaps:	2

US-10-032-254A-1 (1-1554) x US-10-090-002-4 (1-370)

QY 120 AAACAGACGGAGGACATCAGCAGTGTCTATGATCCGGGAGAGCTGGGCTCGGTGCC 179

Db 11 LysGlnAlaGluAspIleArgAspIleTyrAspPheArgAspValLeuGlyThrGlyAla 30

QY 180 TTCTCTGAGGTGATGTGGCCCCAGGAAAGGGCTCTGCTCATCTTGTGGCCTCAAGTGC 239

Db 31 PheSerGluValIleLeuAlaGluAspLysArgThrGlnLysLeuValAlaIleLysCys 50

QY 240 ATTCCCAAGAAAGCACTTCGGGGCAAGGAGGCCCTGGTGGAGAATGAGATCGCGGTACTT 299

Db 51 IleAlaLysGluAlaLeuGluGlyLysGluGlySerMetGluAsnGluIleAlaValLeu 70

QY 300 CGCAGAATCAGCCATCCCAACATTGTGGCTCTGGAGGACGTCCATGAGAGTCTTCTCAT 359

Db 71 HisLysIleLysHisProAsnIleValAlaLeuAspAspIleTyrGluSerGlyGlyHis 90

QY 360 CTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAACCTGTTGACCGCATCATGGAGCGG 419

Db 91 LeuTyrLeuIleMetGlnbeuValSerGlyGlyGluPheAspArgIleValGluLys 110

QY 420 GGCTCCTACACAGAGAGGACGCCAGCCACCTTGTAGGGCAGGTCTTGGCGTGTCTCC 479

Db 111 GlyPheTyrThrGluArgAspAlaSerArgLeuIlePheGlnValLeuAspAlaValLys 130

QY 480 TACCTTCATAGCCTGGGCATCGTGCACCGGACCTCAAGCCTGAAAACCTCCTCTATGCC 539

Db 131 TyrLeuHisAspLeuGlyIleValHisArgAspLeuLysProGluAsnLeuLeuTyrTyr 150

QY 540 ACACCTTTTGAGGACTCCAGATCATGGTCTCTGACTTTGGCCTGTCCAAAATACAA--- 596

Db 151 SerLeuAspGluAspSerLysIleMetIleSerAspPheGlyLeuSerLysMetGluAsp 170

QY 597 GCTGGCAACATGCTAGGCACAGCCTGTGGGACCCCGAGGATATGTGGCCCCAGAGCTCCTG 656

Db 171 ProGlySerValLeuSerThrAlaCysGlyThrProGlyTyrValAlaProGluValLeu 190

QY 657 GAGCAGAAACCTACGGGAAGCCGTAGATGTGTGGGCCCTGGGTGTCATCTCCTACATC 716

Db 191 AlaGlnLysProTyrSerLysAlaValAspCysTrpSerIleGlyValIleAlaTyrIle 210

QY 717 CTGCTGTGTGGGTACCCCCCTTCTATGATGAGAGCGATCTGAACTCTTCAGCCAGATT 776

Db 211 LeuLeuCysGlyTyrProPheTyrAspGluAsnAspAlaLysLeuPheGluGlnIle 230

QY 777 CTGAGGGCCAGCTATGAGTTTGACTCCCCCTTTTGGGATGACATCTCAGAAATCAGCCAAA 836

Db 231 LeuLysAlaGluTyrGluPheAspSerProTyrTrpAspAspIleSerAspSerAlaLys 250

QY 837 GACTTCATTGCCACCTTCTGGAACGTGATCCCCAGAAAGAGTTTCACCTGCCAGCAGGCC 896

Db 251 AspPheIleArgHisLeuMetGluLysAspProGluLysArgPheThrCysGluGlnAla 270

QY 897 CTACAGCATCTTTGGATCTCTGGGGATGCAGCCTTCGATAGGACATCCTGGGTTCTGTC 956

Db 271 LeuGlnHisProTrpIleAlaGlyAspThrAlaLeuAspLysAsnIleHisGlnSerVal 290

QY 957 AGTGAGCAGATCCAGAAGAATTTTGGCAGGACCCACTGGAAGCGTGCATTCAATGCCACA 1016

Db 291 SerGluGlnIleLysLysAsnPheAlaLysSerLysTrpLysGlnAlaPheAsnAlaThr 310

QY 1017 TCATTCTACGTACATCCGTAAG-----CTGGGACAAAGCCCGAGGGTGAG 1064

Db 311 AlaValValArgHisMetArgLysLeuGlnLeuGlyThrSerGlnGluGlyGln 328

RESULT 10

US-10-204-041-10

; Sequence 10, Application US/10204041

; Publication No. US20030176443A1

; GENERAL INFORMATION:

; APPLICANT: STEIN-GERLACH, MATTHIAS

; APPLICANT: SALASSIDIS, KONSTADINOS

; APPLICANT: BACHER, GERALD

; APPLICANT: MULLER, STEFAN

; TITLE OF INVENTION: Pyridylpyrimidine Derivatives as Effective Compounds Against Pri

; TITLE OF INVENTION: Infections and Prion Diseases

; FILE REFERENCE: AXM-007.1P US

; CURRENT APPLICATION NUMBER: US/10/204,041

; CURRENT FILING DATE: 2002-08-16

; PRIOR APPLICATION NUMBER: EP 01111858.5

; PRIOR FILING DATE: 2001-05-16

; PRIOR APPLICATION NUMBER: PCT/EP02/05420

; PRIOR FILING DATE: 2002-05-16

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 10

; LENGTH: 370

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-204-041-10

Alignment Scores:

Pred. No.:	1.32e-85	Length:	370
Score:	1184.50	Matches:	220
Percent Similarity:	85.53%	Conservative:	52
Best Local Similarity:	69.18%	Mismatches:	43
Query Match:	41.24%	Indels:	3
DB:	14	Gaps:	2

US-10-032-254A-1 (1-1554) x US-10-204-041-10 (1-370)

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QY 420 GGCTCCTACACAGAGAAGGACGCCACCTTGTAGGGCAGGTCCCTTGGCGCTGTCTCC 479  
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; Sequence 6, Application US/10649400  
; Publication No. US20040110198A1  
; GENERAL INFORMATION:  
; APPLICANT: Bunney Jr., William E.  
; APPLICANT: Jones, Edward G.  
; APPLICANT: Molnar, Margherita  
; APPLICANT: The Board of Trustees of The Leland Stanford  
; APPLICANT: Junior University  
; TITLE OF INVENTION: Genes Involved in Neuropsychiatric Disorders  
; FILE REFERENCE: 020885-000720US  
; CURRENT APPLICATION NUMBER: US/10/649,400  
; CURRENT FILING DATE: 2003-08-26  
; PRIOR APPLICATION NUMBER: US 60/406,879

; PRIOR FILING DATE: 2002-08-28  
; PRIOR APPLICATION NUMBER: US 60/451,306  
; PRIOR FILING DATE: 2003-02-27  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 370  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: calcium/calmodulin dependent protein kinase I  
; OTHER INFORMATION: (CAWKI)  
US-10-649-400-6  
Alignment Scores:  
Pred. No.: 1.32e-85 Length: 370  
Score: 1184.50 Matches: 220  
Percent Similarity: 85.53% Conservative: 52  
Best Local Similarity: 69.18% Mismatches: 43  
Query Match: 41.24% Indels: 3  
DB: 16 Gaps: 2  
US-10-032-254A-1 (1-1554) x US-10-649-400-6 (1-370)  
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; Sequence 36, Application US/09935464  
; Publication No. US20030027153A1  
; GENERAL INFORMATION:  
; APPLICANT: Meyer, Joanne  
; APPLICANT: Barrington-Martin, Rory  
; APPLICANT: Parker, Alexander  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING NEUROPSYCHIA  
; TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA  
; FILE REFERENCE: 3322/1H702 US1  
; CURRENT APPLICATION NUMBER: US/09/935,464  
; CURRENT FILING DATE: 2001-08-23  
; PRIOR APPLICATION NUMBER: US 09/757,300  
; PRIOR FILING DATE: 2001-01-09  
; NUMBER OF SEQ ID NOS: 90  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 36  
; LENGTH: 317  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
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Alignment Scores:  
Pred. No.: 1.82e-85 Length: 317  
Score: 1182.50 Matches: 220  
Percent Similarity: 85.49% Conservative: 51  
Best Local Similarity: 69.40% Mismatches: 43  
Query Match: 41.17% Indels: 3  
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Db 121 TyrLeuHisAspLeuGlyIleValHisArgAspLeuLysProGluAsnLeuTyrTyr 140  
QY 540 ACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTGGCCTGTCCAAAATACAA--- 596  
Db 141 SerLeuAspGluAspSerLysIleMetIleSerAspPheGlyLeuSerLysMetGluAsp 160  
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; Sequence 36, Application US/10125835  
; Publication No. US20030092019A1  
; GENERAL INFORMATION:  
; APPLICANT: Meyer, Joanne  
; APPLICANT: Barrington-Martin, Rory  
; APPLICANT: Parker, Alexander  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING  
; TITLE OF INVENTION: NEUROPSYCHIATRIC  
; TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA  
; FILE REFERENCE: 3322/OH702 US0  
; CURRENT APPLICATION NUMBER: US/10/125,835  
; CURRENT FILING DATE: 2002-04-19  
; PRIOR APPLICATION NUMBER: US/09/757,300  
; PRIOR FILING DATE: 2001-01-09  
; NUMBER OF SEQ ID NOS: 50  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 36  
; LENGTH: 317  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-125-835-36  
  
Alignment Scores:  
Pred. No.: 1.82e-85 Length: 317  
Score: 1182.50 Matches: 220  
Percent Similarity: 85.49% Conservative: 51  
Best Local Similarity: 69.40% Mismatches: 43  
Query Match: 41.17% Indels: 3  
DB: 14 Gaps: 2  
  
US-10-032-254A-1 (1-1554) x US-10-125-835-36 (1-317)



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US-10-664-421-55

; Sequence 55, Application US/10664421  
; Publication No. US20040142864A1  
; GENERAL INFORMATION:  
; APPLICANT: BREMER, RYAN  
; APPLICANT: IBRAHIM, PRABHA  
; APPLICANT: KUMAR, ABHINAV  
; APPLICANT: MANDIYAN, VALSAN

; APPLICANT: MILBURN, MICHAEL V.  
; TITLE OF INVENTION: CRYSTAL STRUCTURE OF PIM-1 KINASE  
; FILE REFERENCE: 039363/0703  
; CURRENT APPLICATION NUMBER: US/10/664,421  
; CURRENT FILING DATE: 2003-09-16  
; PRIOR APPLICATION NUMBER: 60/412,341  
; PRIOR FILING DATE: 2002-09-20  
; PRIOR APPLICATION NUMBER: 60/411,398  
; PRIOR FILING DATE: 2002-09-16  
; NUMBER OF SEQ ID NOS: 169  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 55  
; LENGTH: 326  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-664-421-55  
  
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Best Local Similarity: 65.97% Mismatches: 42  
Query Match: 40.96% Indels: 21  
DB: 16 Gaps: 2  
  
US-10-032-254A-1 (1-1554) x US-10-664-421-55 (1-326)  
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Db 313 ThrAlaValValArgHisMetArgLysLeuHisLeuGlySerSerLeuAspSerSerAsn 332  
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Db 333 AlaSer 334

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Job time : 831 secs



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GenCore version 5.1.6  
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Run on: June 5, 2005, 22:42:05 ; Search time 10887 Seconds  
(without alignments)  
6916.451 Million cell updates/sec

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
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3	1454.4	93.6	BC055891 Mus muscu
4	1340.4	86.3	AB004267 Rattus no
5	1261.2	81.2	AR411048 Sequence
6	1032	66.4	AB023027 Mus muscu
7	979.2	63.0	D86556 Rattus norv
8	844.4	54.3	AR139102 Sequence
9	844.4	54.3	AR270390 Sequence
10	836.8	53.8	AX166520 Sequence
11	809	52.1	BC064422 Homo sapi
12	781.6	50.3	CQ728144 Sequence
13	534.4	34.4	AB098710 Xenopus l
14	512	32.9	RATCAMPKAA
15	512	32.9	BC071177 Rattus norv
16	510.4	32.8	BC014825 Mus muscu
17	502.4	32.3	1402 10 RATPRKI
18	500.8	32.2	1113 12 AY335764
19	500.8	32.2	1480 6 AR270891 Sequence

20	500.8	32.2	1480	6	AX601399	AX601399 Sequence
21	500.8	32.2	1480	9	HUMCKI	L41816 Homo sapien
22	461	29.7	2504	5	AY606040	AY606040 Oncorhync
23	454.4	29.2	1149	5	AB083000	AB083000 Xenopus l
24	450.4	29.0	1506	5	CR761672	CR761672 Xenopus t
25	450.4	29.0	2201	5	BC041721	BC041721 Xenopus l
26	436.2	28.1	1074	6	AR373295	AR373295 Sequence
27	436.2	28.1	1074	6	AX166517	AX166517 Sequence
28	436.2	28.1	1074	6	AX167587	AX167587 Sequence
29	436.2	28.1	1158	6	AR373294	AR373294 Sequence
30	436.2	28.1	1158	6	AX167585	AX167585 Sequence
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43	430	27.7	1738	9	HS272L161	AL049688 Human gen
44	430	27.7	2464	9	AF428261	AF428261 Homo sapi
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ALIGNMENTS

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AF181984  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
source  
CDS

AF181984  
Mus musculus pregnancy upregulated nonubiquitous  
Ca2+/calmodulin-dependent kinase Pnck mRNA, complete cds.  
AF181984  
AF181984.1 GI:6841607  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 1554)  
Gardner,H.P., Rajan,J.V., Ha,S.I., Copeland,N.G., Gilbert,D.J.,  
Jenkins,N.A., Marquis,S.T. and Chodosh,L.A.  
Cloning, characterization, and chromosomal localization of Pnck, a  
Ca(2+)/calmodulin-dependent protein kinase  
Genomics 63 (2), 279-288 (2000)  
20139438  
10673339  
2 (bases 1 to 1554)  
Gardner,H.P. and Chodosh,L.A.  
Direct Submission  
Submitted (31-AUG-1999) Molecular and Cellular Engineering,  
University of Pennsylvania, 612 BRBII/III, 421 Curie Blvd,  
Philadelphia, PA 19104-6160, USA  
Location/Qualifiers  
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ORIGIN

Query Match 100.0%; Score 1554; DB 10; Length 1554;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1554; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	61	GGTGACTGTGTCGTGACAGGTGGCTGCAAGCAGGGTCGCAGACATGCTGCTCAAGA	120
Db	61	GGTGACTGTGTCGTGACAGGTGGCTGCAAGCAGGGTCGCAGACATGCTGCTCAAGA	120
QY	121	AACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAAGCTCGGCTCGGCT	180
Db	121	AACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAAGCTCGGCTCGGCT	180
QY	181	TCTCTGAGGTGATGCTGGCCCAAGAAAGGSGCTCTGCTCATCTTGTGGCCCTCAAGT	240
Db	181	TCTCTGAGGTGATGCTGGCCCAAGAAAGGSGCTCTGCTCATCTTGTGGCCCTCAAGT	240
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QY	301	GCAGAATCAGCCATCCCAACATTGTGGCTCTGGAGGACGTCATGAGAGTCCTTCTCATC	360
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QY	361	TCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAACCTGTTGACCGCATCATGGAGCGGG	420
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QY	421	GCTCCTACACAGAGAAGGACGCGCACCCCTTGTTAGGGCAGGTCTTGGCGCTGTCTCCT	480
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QY	721	TGTGTGGGTACCCCCCTTCTATGATGAGAGCGATCCTGAACCTTTCAGCCAGATTCTGA	780
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QY	1141	CAGGTAGATGCCAAGGAAGGCCAAGTGGACTGACTCCCGGTTTTTCTTCTCCAGCCCT	1200
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QY	1201	TTTGGTCTCTTCTGGATCCTTGTCTCCAGACTGGCCTCTCTGTGAAAGTCTGAGACT	1260
Db	1201	TTTGGTCTCTTCTGGATCCTTGTCTCCAGACTGGCCTCTCTGTGAAAGTCTGAGACT	1260
QY	1261	GGGTGATGATGGCACTAGGGTACGGGGCTTCCCCAGTATGTCCCCCAGCCTCTATTTC	1320
Db	1261	GGGTGATGATGGCACTAGGGTACGGGGCTTCCCCAGTATGTCCCCCAGCCTCTATTTC	1320
QY	1321	TTACCTATGGTGGAGGCTCCCTTTCCCATGTGCGTCCACCCCTCTATGGAACCTGAGGAG	1380
Db	1321	TTACCTATGGTGGAGGCTCCCTTTCCCATGTGCGTCCACCCCTCTATGGAACCTGAGGAG	1380
QY	1381	GTGTTCAAAAGTGGACTTGGGAGCCATCCTTCTGCACCTTGACAAACACATGCTTGT	1440
Db	1381	GTGTTCAAAAGTGGACTTGGGAGCCATCCTTCTGCACCTTGACAAACACATGCTTGT	1440
QY	1441	GTGGCTGTCTGTGCTTTGCTGACTGTGGTGGTCTGCTGTGTGTGGCCCTTTAGTT	1500
Db	1441	GTGGCTGTCTGTGCTTTGCTGACTGTGGTGGTCTGCTGTGTGTGTGGCCCTTTAGTT	1500
QY	1501	CCTCCTTTTCTTAACCAATAAAGACAAACAGAACCAAAAAA	1554
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RESULT 2	BC051996	1498 bp	mRNA	linear	ROD 16-SEP-2003
LOCUS	Mus musculus pregnancy upregulated non-ubiquitously expressed Cam				
DEFINITION	kinase, mRNA (cdna clone IMAGE:5693661), partial cds.				
ACCESSION	BC051996				
VERSION	BC051996.1 GI:30704685				
KEYWORDS	Mus musculus (house mouse)				
SOURCE	Mus musculus				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 1498)				
AUTHORS	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,				



Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.  
Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
22388257  
12477932  
2 (bases 1 to 1498)  
Strausberg,R.  
Direct Submission  
Submitted (01-MAY-2003) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
NIH-MGC Project URL: http://mgc.nci.nih.gov  
Contact: MGC help desk  
Email: cgabbs-r@mail.nih.gov  
Tissue Procurement: Dr. Jim Lin, University of Iowa  
cDNA Library Preparation: M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Sequencing Group at the Stanford Human Genome  
Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: http://www-shgc.stanford.edu  
Contact: (Dickson, Mark) mcd@paxil.stanford.edu  
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,  
R. M.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
Series: IRAK Plate: 114 Row: c Column: 16  
This clone was selected for full length sequencing because it  
passed the following selection criteria: matched mRNA gi: 6753247.

FEATURES

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ORIGIN

Query Match 93.7%; Score 1455; DB 10; Length 1498;  
Best Local Similarity 100.0%; Pred.No. 0;  
Matches 1456; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3  
BC055891  
LOCUS BC055891 1489 bp mRNA linear ROD 30-JUN-2004  
DEFINITION Mus musculus pregnancy upregulated non-ubiquitously expressed Cam kinase, mRNA (cdna clone MGC:68193 IMAGE:4208888), complete cds.  
ACCESSION BC055891  
VERSION BC055891.1 GI:33585934  
KEYWORDS MGC.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 1489)  
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

TITLE human and initial analysis of more than 15,000 full-length human and mouse cdna sequences  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
PUBMED 12477932  
REFERENCE 2 (bases 1 to 1489)  
AUTHORS Strausberg,R.  
TITLE Direct Submission  
JOURNAL Submitted (01-AUG-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA  
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
COMMENT Contact: MGC help desk  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Jeffrey E. Green, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: <http://www-shgc.stanford.edu>  
Contact: (Dickson, Mark) [mcd@paxil.stanford.edu](mailto:mcd@paxil.stanford.edu)  
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAK Plate: 120 Row: j Column: 1  
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Rattus.  
REFERENCE 1 (sites)  
AUTHORS Naito,Y., Watanabe,Y., Yokokura,H., Sugita,R., Nishio,M. and  
Hidaka,H.  
TITLE Isoform-specific activation and structural diversity of calmodulin  
kinase I  
JOURNAL J. Biol. Chem. 272 (51), 32704-32708 (1997)  
MEDLINE 98070455  
PUBMED 9405489  
REFERENCE 2 (bases 1 to 1618)  
AUTHORS Naito,Y.  
TITLE Direct Submission  
JOURNAL Submitted (23-MAY-1997) Yasuhito Naito, Nagoya University School of  
Medicine, Department of Pharmacology; 65 Tsurumai-cho, Showa-ku,  
Nagoya 466, Japan (E-mail:ynaito@tsuru.med.nagoya-u.ac.jp,  
Tel:+81-52-744-2076, Fax:+81-52-744-2083)  
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REFERENCE 1 (bases 1 to 1458)  
AUTHORS Sutcliffe,J.G., Gautvik,K.M., De Lecea,L., Bloom,F.E.,  
Danielson,P.E., Gautvik,V.T., Kilduff,T.S. and Foye,P.E.  
TITLE Hypothalamus-specific polypeptides  
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Db 1397 TGCTTGTGTGTAGCCCTTTAGTTCCCTCCTTTTCCAAACCAATAAAGACAAACAGAACAA 1456  
RESULT 6  
AB023027  
LOCUS AB023027 1032 bp mRNA linear ROD 04-DEC-1999  
DEFINITION Mus musculus mCaMK1-beta2 mRNA, complete cds.  
ACCESSION AB023027  
VERSION AB023027.1 GI:6525258  
KEYWORDS mCaMK1-beta2.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 1032)  
AUTHORS Ueda,T. and Minami,Y.  
TITLE mCaMK1-beta2  
JOURNAL Published Only in DataBase (1999)  
REFERENCE 2 (bases 1 to 1032)  
AUTHORS Ueda,T. and Minami,Y.  
TITLE Direct Submission  
JOURNAL Submitted (29-JAN-1999) Takahiro Ueda, Kobe University School of  
Medicine, Dep of Biochemistry; 7-5-1, Kusunoki-Cho,Chuo-Ku, Hyogo  
650-0017, Japan (E-mail:uedat@med.kobe-u.ac.jp,  
Tel:81-78-341-7451(ex.3251), Fax:81-78-371-8734)  
FEATURES  
Location/Qualifiers  
1..1032  
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ORIGIN  
Query Match 66.4%; Score 1032; DB 10; Length 1032;  
Best Local Similarity 100.0%; Pred. No. 3.8e-260;  
Matches 1032; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 105 ATGCTGCTGCTCAAGAAAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAAG 164  
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QY 165 CTGGGCTCGGGTGCCTTCTCTGAGGTGATGTGCGCCCAAGAAAGGGCTCTGCTCATCTT 224  
Db 61 CTGGGCTCGGGTGCCTTCTCTGAGGTGATGTGCGCCCAAGAAAGGGCTCTGCTCATCTT 120  
QY 225 GTGGCCCTCAAGTGCATTTCCCAAGAAAGCACTTCGGGGCAAGGAGGCCCTGTGGAGAAAT 284  
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Db 181 GAGATCGCGGTACTTCGCAGAATCAGCCATCAGCCATCCCAACATTTGGTCTCTGGAGACGTCCAT 240  
QY 345 GAGAGTCCTTCTCATCTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAACCTTTTGAC 404  
Db 241 GAGAGTCCTTCTCATCTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAACCTTTTGAC 300  
QY 405 CGCATCATGGAGCGGGGCTCCTACACAGAGAAGGACGCCAGCCACCTTGTAGGCAGGTC 464

Db 301 CGCATATGGAGCGGGCTCCTACACAGAGAAGGACGCCAGCACCTTGTAGGGCAGGTC 360

Qy 465 CTTGGCGCTGTCTCCTACCTTCATAGCCTGGGCATCGTGCAACCGGACCTCAAGCCCTGAA 524  
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Qy 525 AACCTCTCTATGCCACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTGGCCCTG 584  
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Db 421 AACCTCTCTATGCCACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTGGCCCTG 480  
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Db 721 GAATCAGCCAAAGACTTTCATTGCGCCACCTTCTGGAACGTGATCCCAGAAAGGTTTCACC 780  
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Qy 885 TGCCAGCAGCGCCCTACAGCATCTTTGGATCTCTGGGATGCAGCCTTCGATAGGGACATC 944  
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Db 901 TTCAATGCCACATCATTCCTACGTCACATCCGTAAGCTGGGACAAAGCCCAGAGGGTGAG 960  
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Qy 1065 GAGGCCTCCAGGCAGTGTATGACCCGTCATAGCCACCCAGGCCCTTGGGACTAGCCAGTCC 1124  
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Db 961 GAGGCCTCCAGGCAGTGTATGACCCGTCATAGCCACCCAGGCCCTTGGGACTAGCCAGTCC 1020  
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Qy 1125 CCCAAGTGGTGA 1136  
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Db 1021 CCCAAGTGGTGA 1032  
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RESULT 7

D86556  
LOCUS D86556 1332 bp mRNA linear ROD 07-FEB-1999

DEFINITION Rattus norvegicus mRNA for Protein Kinase, complete cds.

ACCESSION D86556

VERSION D86556.1 GI:2077931

KEYWORDS Protein Kinase.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 1332)

AUTHORS Yokokura,H., Terada,O., Naito,Y. and Hidaka,H.

TITLE Isolation and comparison of rat cDNAs encoding Ca2+/calmodulin-dependent protein kinase I isoforms

JOURNAL Biochim. Biophys. Acta 1338 (1), 8-12 (1997)

MEDLINE 97228532

PUBMED 9074610

REFERENCE 2 (bases 1 to 1332)

AUTHORS Yokokura,H.

TITLE Direct Submission

JOURNAL Submitted (15-JUL-1996) Hisayuki Yokokura, Nagoya University School of Medicine, Department of Pharmacology; Tsurumai 65, Showa-ku, Nagoya, Aichi 466, Japan (Tel:052-744-2075, Fax:052-744-2083)

FEATURES

source Location/Qualifiers

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/clone="N2 and N25"

/tissue\_type="Brain"

/clone\_lib="S. Nakanishi"

/dev\_stage="embryo (E18)"

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66..1094

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polyA\_signal 1315..1320

polyA\_site 1332

/note="19 a nucleotides"

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Query Match 63.0%; Score 979.2; DB 10; Length 1332;

Best Local Similarity 84.7%; Pred. No. 2.9e-246;

Matches 1218; Conservative 0; Mismatches 53; Indels 167; Gaps 4;

QY 99 GCAGACATGCTGCTGCTCAAGAAACAGACGAGGACATCAGCAGTGTCTATGAGATCCGG 158  
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Db 60 GCAGACATGCTGCTGCTCAAGAAACAGACGAGGACATCAGCAGTGTCTATGAGATCCGG 119  
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QY 159 GAGAACCTGGGCTCGGGTGCCTTCTCTGAGGTGATGCTGGCCCCAGGAAAGGGCTCTGCT 218  
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Db 120 GAGAACCTGGGCTCGGGTGCCTTCTCTGAGGTGATGCTGGCCCCAGGAAAGGGCTCTGCT 179  
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QY 219 CATCTTGTGGCCCTCAAGTGCATTCCCAAGAAAGCACTTCGGGGCAAGAGGCCCTGGTG 278  
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Db 180 CATCTTGTGGCCCTCAAGTGCATTCCCAAGAAAGCACTTCGGGGCAAGAGGCCCTGGTG 239  
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QY 279 GAGAAATGAGATCGCGGTACTTCGCAGAAATCAGCCATCCCAACATTTGTGGCTCTGGAGGAC 338  
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Db 240 GAGAAATGAGATCGCAGTACTCCGCAAGATTAGCCACCCCAACATTTGTGGCTCTGGAGGAC 299  
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QY 339 GTCCATGAGAGTCCTTCTCATCTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAACCTG 398  
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Db 300 GTCCACGAGAGCCCTTCCCATCTCTACTTTGGCCATGGAGCTGGTAACAGGTGGTGAACCTG 359  
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QY 399 TTTGACCCGCATCATGGAGCGGGCTCCTACACAGAGAAGGACGCCAGCCACCTTGTAGGG 458  
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Db 360 TTTGACCGAAATCATGGAGCGGGCTCCTACACAGAGAAGGATGCGAGCCACCTTGTAGGG 419  
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QY 519 CCTGAAAACCTCCTCTATGCCACACCTTTTGAGGACTCCAAGATCATGTGCTCTGACTTT 578  
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Db 480 CCTGAAAACCTCCTCTATGCCACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTT 539  
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QY 579 GGCCTGTCCAAAAATACAAGCTGGCAACATGCTAGGCACAGCCTGTGGGACCCAGGATAT 638  
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Db 540 GGCCTGTCCAAAAATTCAAGCTGGCAACATGCTAGGCACAGCCTGTGGGACCCAGGATAT 599  
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QY 639 GTGGCCCCAGAGCTCCTGGAGCAGAAACCTACGGGAAGCCGCTAGATGTGTGGGCCCTGT 698  
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Db 600 GTGGCCCCAGAGCTCTGGAGCAGAAACCCCTACGGGAAGCGCGTAGATGTGTGGCCCTG 659  
QY 699 GGTGTATCTCTACATCTCTGCTGTGTGGTACCCCCCTTCTATGATGAGACGATCCT 758  
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QY 759 GAACTCTTCAGCCAGATTCTGAGGGCCAGCTATGAGTTTGACTCCCTTTTGGGATGAC 818  
Db 720 GAACTCTTCAGCCAGATTCTGAGGGCCAGCTACGAGTTTGACTCTCCCTTTTGGGATGAC 779  
QY 819 ATCTCAGATCAGCCAAAGACTTCATTGCCACCTTCTGGAACGTGATCCCCAGAAAGG 878  
Db 780 ATCTCAGATCAGCCAAAGACTTCATTCCGACCTTCTGGAACGTGATCCCCAGAAAGG 839  
QY 879 TTCACCTGCCAGAGGCCCTACAGCATCTTTGGATCTCTGGGGATGAGCCTTCGATAGG 938  
Db 840 TTCACCTGCCAAAGGCCCTTACAGCATCTCTGGATCTCTGGGGATGAGCCTTTGGACAGG 899  
QY 939 GACATCTTGGTCTGTGAGTGAGCAGATCCAGAAAGATTTTGCCAGGACCCACTGGAAG 998  
Db 900 GACATCTTAGTCTGTGAGTGAGCAGATCCAGAAAGATTTTGCCAGGACCCACTGGAAG 959  
QY 999 CGTGCAATCAATGCCACATCATTCCTACGTACATCCGTAAGCTGGGACAAAGCCCAGAG 1058  
Db 960 CGTGCAATCAATGCCACATCATTCCTACGTACATCCGTAAGCTGGGACAGAGCCCAGAG 1019  
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QY 1357 CCACCTCTATGGAACCTGAGGAGGTGTTCAAAAGTGGACTTGGGAGCCATCCTTCCTGC 1416  
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RESULT 8  
LOCUS AR139102 1282 bp DNA linear PAT 16-JUN-2001  
DEFINITION Sequence 12 from patent US 6207148.  
ACCESSION AR139102  
VERSION AR139102.1 GI:14481598  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1282)  
AUTHORS Bandman,O., Hillman,J.L., Corley,N.C., Guegler,K.J., Lal,P., Goli,S.K. and Shah,P.

TITLE Disease associated protein kinases  
JOURNAL Patent: US 6207148-A 12 27-MAR-2001;  
FEATURES Location/Qualifiers  
source 1..1282  
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Query Match 54.3%; Score 844.4; DB 6; Length 1282;  
Best Local Similarity 86.2%; Pred. No. 8.6e-211;  
Matches 940; Conservative 1; Mismatches 145; Indels 4; Gaps 1;  
QY 101 AGACATGCTGCTGCTCAAGAAACACAGACGAGGACATCAGCAGTGTCTATGAGATCCGGGA 160  
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Db 257 GAGGCTCGGCTCGGCTGCCCTTCTCCGAGGTGGTGTGGCCACAGGACGCGGGCTCCGCACA 316  
QY 221 TCTTGTGGCCCTCAAGTGCAATCCCAAGAAACACTTCGGGGCAAGGAGGCCCTGGTGA 280  
Db 317 CCTCGTGGCCCTCAAGTGCAATCCCAAGAAAGGCCCTCCGGGGCAAGGAGGCCCTGGTGA 376  
QY 281 GAATGAGATCGCGGTACTTCGCAGAAATCAGCCATCCCAACATTGTGGTCTTGAGGACGT 340  
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QY 341 CCATGAGAGTCTTCTCATCTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAACCTGTT 400  
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QY 401 TGACCCGATCATGGAGCGGGCTCTTACACAGAGAAAGACGCGCCAGCCACCTTGTAGGGCA 460  
Db 497 TGACCCGATCATGGAGCGGGCTCTTACACAGAGAAAGGATGCCAGCCATCTGGTGGGTCA 556  
QY 461 GGTCTTTGGCGCTGTCTCCTACCTTATAGCCTGGGCATCGTGCACCGGACCTCAAGCC 520  
Db 557 GGTCTTTGGCGCGCTCTCCTACCTGCACAGCCTGGGGATCGTGCACCGGACCTCAAGCC 616  
QY 521 TGAACACCTCCTCTATGCCACACCTTTTGAGGACTCCAAGATCATGTGCTCTGACTTTGG 580  
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QY 581 CCTGTCCAAAATACAAGCTGGCAACATGCTAGGCACAGCCTGTGGACCCAGGATATGT 640  
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QY 701 TGTATCTCTCATCTGTGTGGTACCCCTTCTATGATGAGAGCGATCCTGA 760  
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LOCUS AR270390 1282 bp DNA linear PAT 10-APR-2003  
DEFINITION Sequence 953 from patent US 6500938.  
ACCESSION AR270390  
VERSION AR270390.1 GI:29701624  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 1282)  
AUTHORS Au-Young,J. and Seilhamer,J.J.  
TITLE Composition for the detection of signaling pathway gene expression  
JOURNAL Patent: US 6500938-A 953 31-DEC-2002;  
FEATURES  
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Query Match 54.3%; Score 844.4; DB 6; Length 1282;  
Best Local Similarity 86.2%; Pred. No. 8.6e-211;  
Matches 940; Conservative 1; Mismatches 145; Indels 4; Gaps 1;  
Qy 101 AGACATGCTGCTCAAGAAACAGACGAGGACATCAGCAGTGTCTATGATCCGGGA 160  
Db 197 AAACATGCTGCTGAAGAAACACACGGAGGACATCAGCAGCGTCTACGAGATCCGCGA 256  
Qy 161 GAAGCTGGGTCGGGTGCCTTCTCTGAGTGATGTGGCCCAAGGAAGGGGCTCTGCTCA 220  
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Qy 1061 TGAGGAGGCCCTCCAGGCAGTGTATGACCCCGTCATAGCCACCCAGGCCCTTGGGACTAGCCA 1120  
Db 1157 CGAGGGGCGCTCTGAGCAGGGCATGGSCCGNCACAGCCACTNAGGCCCTCGTGTGGCCA 1216  
Qy 1121 GTCCCCCAAGTGGTGAAACCAGGTAGATGCCAAGGAAGGCCAAGTGGACTGACTCCCGG 1180  
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Qy 1181 TTTTCTTTC 1190  
Db 1273 ATTTNCTTNC 1282  
RESULT 10  
AX166520  
LOCUS AX166520 1032 bp DNA linear PAT 22-JUN-2001  
DEFINITION Sequence 11 from Patent WO0138503.  
ACCESSION AX166520  
VERSION AX166520.1 GI:14546865  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
REFERENCE 1  
AUTHORS Plowman,G.D., Whyte,D., Manning,G.S., Sudarsanam,S.S., Martinez,R.,  
Flanagan,P. and Clary,D.S.  
TITLE Novel human protein kinases and protein kinase-like enzymes  
JOURNAL Patent: WO 0138503-A 11 31-MAY-2001;  
FEATURES  
source location/Qualifiers  
1. .1032  
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ORIGIN  
Query Match 53.8%; Score 836.8; DB 6; Length 1032;  
Best Local Similarity 88.2%; Pred. No. 8.5e-209;  
Matches 910; Conservative 0; Mismatches 122; Indels 0; Gaps 0;  
Qy 105 ATGCTGCTGCTCAAGAAACAGACGCGGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAAG 164





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/lab\_host="DH10B"  
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/note="synonym: MGC45419"  
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QALRHLWISGDTAFDRDILGSVSEQIRKNFARTHWKRAFNAFSLRHIRKLGQIPEGE  
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ORIGIN

Query Match		52.1%;	Score 809;	DB 9;	Length 1624;
Best Local Similarity		74.1%;	Pred. No. 1.8e-201;		
Matches 1168;		Conservative	0;	Mismatches 275;	Indels 134; Gaps 6;
Qy	101	AGACATGCTGCTCAAGAAACAGACGAGGACATCAGCAGTGTCTATGAGATCCGGGA	160.		
Db	17	AGACATGCTGCTGAAGAAACACACGAGGAGACATCAGACGCTACGAGATCCCGGA	76		
Qy	161	GAAGCTGGCTCGGGTGCCCTTCTCTGAGTGATGCTGGCCCCAGGAAAGGGGCTCTGCTCA	220		
Db	77	GAGGCTCGGTCGGGTGCCCTTCTCCGAGGTGGTGTCTGGCCCCAGGAGCGGGGCTCCGCACA	136		
Qy	221	TCTTGTGGCCTCAAGTGCAATCCCAAGAAAGCACTTCGGGGCAAGGAGGCCCTTGGTGA	280		
Db	137	CCTCGTGGCCTCAAGTGCAATCCCAAGAAAGGCCCTCCGGGGCAAGGAGGCCCTTGGTGA	196		
Qy	281	GAATGAGATCGCGGTACTTCGCAGAAATCAGCCATCCCAACATTGGCTCTGGAGGACGT	340		
Db	197	GAACGAGATCGCAGTGCTCCGTAGGATCAGTCACCCCAACATCGTCGCTCTGGAGGATGT	256		
Qy	341	CCATGAGAGTCCTTCTCATCTCTACTTGGCCATGGAGCT	379		
Db	257	CCACGAGAGCCCTTCCCACCTCTACCTGGCCATGGAACTGTGAGGAGGGCCTGGGCAGGC	316		
Qy	380	-----	379		
Db	317	TGTGGAGCCGGGAGGGACTGAGCAGTGAGTGGGGCTGAAGSCCAGGCTGAGTGCCTGG	376		
Qy	380	-----GGTAACAGGTGGTGAACCTGTTTGACCCGCATCATG	413		
Db	377	GTCAGCCAAACCCCTGGCACCCCCAGGGTGACGGGTGGCGAGCTGTTGACCGCATCATG	436		
Qy	414	GAGCGGGGCTCTACACAGAGAAGGACGCCAGCCACCTTGTAGGGCAGGTCCCTTGGCGCT	473		
Db	437	GAGCGCGGCTCCTACACAGAGAAGGATGCCAGCCATCTGGTGGGTGAGGTCTTGGCGCC	496		
Qy	474	GTCTCCTACCTTCATAGCCTGGGCATCTGCACCGGGACCTCAAGCCTGAAGAACCTCCTC	533		
Db	497	GTCTCCTACCTGCACAGCCTGGGGATCGTGACCGGGACCTCAAGCCGAAAAACCTCCTG	556		
Qy	534	TATGCCACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTGGCCTGTCCAAAAATA	593		
Db	557	TATGCCACGCCCTTTGAGGACTCGAAGATCATGGTCTCTGACTTTGGACTCTCCAAAAATC	616		
Qy	594	CAAGCTGGCAACATGCTAGGCACAGCCTGTGGACCCCGAGGATATGTGGCCCCAGAGCTC	653		
Db	617	CAGGCTGGGAACATGCTAGGCACCGCCTGTGGACCCCTTGGATATGTGSCCCAGAGCTC	676		
Qy	654	CTGGAGCAGAAACCCCTACGGGAAGCCGTAGATGTGTGGGCCCTGGGTGTCTATCTCCTAC	713		
Db	677	TTGGAGCAGAAACCCCTACGGGAAGCCGTAGATGTGTGGGCCCTGGGCGTCAATCTCCTAC	736		

Qy	714	ATCCTGCTGTGGGTACCCGCCCTTCTATGATGAGAGCGATCCTGAACTCTTCAGCCAG	773
Db	737	ATCCTGCTGTGGGTACCCGCCCTTCTACGACGAGAGCGACCTTGAGCTCTTCAGCCAG	796
Qy	774	ATTCTGAGGGCCAGCTATGAGTTTGACTCCCCCTTTTGGGATGACATCTCAGAATCAGCC	833
Db	797	ATCCTGAGGGCCAGCTATGAGTTTGACTCTCCTTTCTGGGATGACATCTCAGAATCAGCC	856
Qy	834	AAAGACTTCATTCCGCCACCTTCTGGAACGTGATCCCCAGAAAGAGGTTACCTGCCAGCAG	893
Db	857	AAAGACTTCATCCGGCACCTTCTGGAGCGAGACCCCCAGAAAGAGGTTACCTGCCAACAG	916
Qy	894	GCCCTACAGCATCTTTGGATCTCTGGGGATGCAGCCTTCGATAGGGACATCCTGGGTTCT	953
Db	917	GCCTTCCGGCACCTTTGGATCTCTGGGGACACAGCCTTCGACAGGACATCTTAGGCTCT	976
Qy	954	GTCAGTGAGCAGATCCAGAAGAAATTTTGCAGGACCCACTGGAAAGCGTGCAATCAATGCC	1013
Db	977	GTCAGTGAGCAGATCCGGAAGAACTTTGCTCGGACACACTGGAAGCGAGCCTTCAATGCC	1036
Qy	1014	ACATCATTCCTACGTCACATCCGTAAGCTGGGACAAAAGCCCCAGAGGCTGAGGAGCCTCC	1073
Db	1037	ACCTCGTTCTTGGCCACATCCGGAAGCTGGGCAGATCCCAGAGGGGAGGGGCTCT	1096
Qy	1074	AGGCATGTATGACCCGTCATAGCCACCCAGGCCCTTGGGACTAGCCAGTCCCCCAAGTGG	1133
Db	1097	GAGCAGGCGATGGCCCGCCACAGCCACTCAGGCCCTCCGTGCTGGCCAGCCCCCAAGTGG	1156
Qy	1134	TGAACACCAAGGTAGATGCCAAGGAAGGCCAAGTGGACTGACTCCCGGTTTTTCTTCCTC	1193
Db	1157	TGATGCCCAGGCAGATGCC----GAGGCCAAGTGGACTGACCCCCAGATTTCTTCCCTT	1212
Qy	1194	CAGCCCTTTTGGTCTCTTTCCCTGGATCCTTGTCTCCAGACTGGCCTCTGCTGGAAGTC	1253
Db	1213	GGATGCTTTCGGTCCCTTCCCCCAACCCCTCCCCCTGGGGCTGGCCTCTGCTGGATTTG	1272
Qy	1254	TGAGA-CTGGGTGTGATGATGGCACTAGGGT----ACGGGGCTTCCCCAGTATGTCCTCC	1308
Db	1273	AGATTTGAGGGTGTGGCGCATGGCGCTGGGGTTGGAATGGGGCACCCCCAAGTCTGTCCC	1332
Qy	1309	CAGCCTCTATTCTTACCTATGGTGGAGGCTCCCTTTCCCATGTGCTGCCACCCCTCTATG	1368
Db	1333	CAGGCTCTGCCCTGCCCTGGGGGAGTGCTCCCTCCCTCTTTCCTCTTCCCGCCCTGC	1392
Qy	1369	GAACTGAGGAGGTGTTCAAAAGTGGACTTGGAGCCATCCTTCTGACACCTTGACAGAA	1428
Db	1393	CCCCCGCCCCGCCAAAGCCGAGGGGGTGTGGCAGGGGGGCTCAGGGGCTGTCTTT	1452
Qy	1429	CACATGCAATTGTGGCTGTTCTGTGCTTTGCTGACTGTGGGTGGTCTGCTTGTGTTGT	1488
Db	1453	CC-----TGACAGGCTGTTGTGTGCTTCGCTGAGTGTGGGTGGTCTGCTGTGTGTCAT	1505
Qy	1489	GGCCCTTTAGTTCTCTCC-----TTTTTCTTAAACCAATAAAGACAAACAGAACCAA	1537
Db	1506	GGTCATGGCCTTCCAGCCCCCTCCAGTTTTCCTCCAAACCAATAAAGAAAGATACAGCAA	1565
Qy	1538	AAAAAAAAAAAAAAAAAAAA	1554
Db	1566	AAAAAAAAAAAAAAAAAAAA	1582

RESULT 12					
CQ728144					
LOCUS	CQ728144	964 bp	DNA	linear	PAT 03-FEB-2004
DEFINITION	Sequence 14078 from Patent WO02068579.				
ACCESSION	CQ728144				
VERSION	CQ728144.1 GI:42296190				
KEYWORDS	.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				

REFERENCE 1  
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.  
TITLE Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof  
JOURNAL Patent: WO 02068579-A 14078 06-SEP-2002;  
PE Corporation (NY) (US)  
FEATURES Location/Qualifiers  
source 1. .964  
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ORIGIN  
Query Match 50.3%; Score 781.6; DB 6; Length 964;  
Best Local Similarity 88.2%; Pred. No. 2.8e-194;  
Matches 850; Conservative 0; Mismatches 114; Indels 0; Gaps 0;  
QY 173 GGGTGCCTTCTCTGAGGTGATGCTGGCCCCAGGAAGGGGCTCTGCTCATCTTTGGGCCCT 232  
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Db 1 GGGTGCCTTCTCCGAGGTGCTGGCCCCAGGAGCGGGCTCCGCACACCTCTGTGGCCCT 60  
QY 233 CAAAGTGCATTTCCCAAGAAAGCACTTCGGGGCAAGGAGCCCTGGTGGAGAAATGAGATCGC 292  
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Db 61 CAAAGTGCATCCCCAAGAGGCCCTCCGGGGCAAGGAGGCCCTGGTGGAGAACGAGATCGC 120  
QY 293 GGTACTTCGCAGAATCAGGCATCCCAACATTTGGTCTCTGGAGGACGTCCATGAGAGTCC 352  
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Db 121 AGTGCTCAGTAGGATCAGTCACCCCAACATCGTCGCTCTGGAGGATGTCCACGAGAGCCC 180  
QY 353 TTCTCATCTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAACCTGTTTGACCGCATCAT 412  
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Db 181 TTCCCACCTCTACCTGGCCATGGAACCTGGTGACGGGTGGCGAGCTGTTTGACCGCATCAT 240  
QY 413 GGAGCGGGGCTCCTACACAGAAAGGACGCCACCTTGTAGGGCAGGTCTCTTGGCGC 472  
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Db 241 GGAGCGGGCTCCTACACAGAAAGGATGCCAGCCATCTGGTGGGTGAGTCTCTTGGCGC 300  
QY 473 TGTCTCCTACCTTATAGCTGGGCATCGTGCACCGGACCTCAAGCCTGAAACCTCCT 532  
Db 301 CGTCTCCTACCTGCACAGCGTGGGATCGTGCACCGGACCTCAAGCCCCGAAACCTCCT 360  
QY 533 CTATGCCACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTTGGCCTGTCCAAAAT 592  
Db 361 GTATGCCACGCCCTTTGAGGACTCGAAGATCATGGTCTCTGACTTTGGAATCTCCAAAAT 420  
QY 593 ACAAGCTGGCAACATGCTAGGCACAGCCCTGTGGGACCCCGAGGATATGTGGCCCCAGAGCT 652  
Db 421 CCAGCTGGGAACATGCTAGGCACCGCCTGTGGGACCCCTGGATATGTGGCCCCAGAGCT 480  
QY 653 CCTGGAGCAGAAACCTTACGGGAAGCCGTAGATGTGTGGGCCCTGGGTGTCTATCTCCTA 712  
Db 481 CTTGGAGCAGAAACCTTACGGGAAGCCGTAGATGTGTGGGCCCTGGGCGTCTATCTCCTA 540  
QY 713 CATCCTGCTGTGGGTACCCCCCTTCTATGATGAGAGCGGATCCTGAACTCTTCAGCCA 772  
Db 541 CATCCTGCTGTGTGGGTACCCCCCTTCTACGACGAGAGCGACCCCTGAGCTCTTCAGCCA 600  
QY 773 GATTCTGAGGGCCAGCTATGAGTTTGAATCCTCCCTTTTGGGATGACATCTCAGAATCAGC 832  
Db 601 GATCCTGAGGGCCAGCTATGAGTTTGAATCTCTCTCTCTTCTGGGATGACATCTCAGAATCAGC 660  
QY 833 CAAAGACTTCATTCCGCCACCTTCTGGAACGTGATCCCCAGAGAGGTTTCACTTCCAGCA 892  
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QY 893 GGCCCTACAGCATCTTTGGATCTCTGGGGATGCAGCCTTCGATAGGGACATCTCTGGGTTTC 952  
Db 721 GGCCTTGGGCACCTTTGGATCTCTGGGACACAGCCTTCGACAGGGACATCTTAGGCTC 780  
QY 953 TGTCAGTGAGCAGATCCAGAGAAATTTTGCCAGGACCCACTGGAAGCGTGTCAATCAATGC 1012  
Db 781 TGTCAGTGAGCAGATCCCGAAGAACTTTGCTCGGACACACTGGAAGCGAGCCITCAATGC 840

QY 1013 CACATCATTTCTACGTACATCCGTAAGCTGGGACAAAGCCCAGAGGCTGAGAGGCCTC 1072  
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Db 841 CACCTCGTTCTTGGCCACATCCCGAAGCTGGGCGAGATCCCAGAGGGCGGCGCCTC 900  
QY 1073 CAGGCAGTGTATGACCCCGTCCATAGCCACCCAGCCCTTGGGACTAGCCAGTCCCCCAAGTG 1132  
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Db 901 TGAGCAGGGCATGGCCGCCACAGCCACTCAGGCCTCCGTGCTGGCCAGCCCCCAAGTG 960  
QY 1133 GTGA 1136  
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Db 961 GTGA 964  
RESULT 13  
AB098710 2831 bp mRNA linear VRT 26-JUN-2003  
LOCUS Xenopus laevis mRNA for Ca2+/calmodulin-dependent protein kinase  
DEFINITION I-like protein, complete cds.  
ACCESSION AB098710  
VERSION AB098710.1 GI:32261077  
KEYWORDS  
SOURCE Xenopus laevis (African clawed frog)  
ORGANISM Xenopus laevis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
Xenopodinae; Xenopus; Xenopus.  
REFERENCE 1  
AUTHORS Kinoshita,S., Sueyoshi,N., Tsuge,T., Suetake,I., Tajima,S. and  
Kameshita,I.  
TITLE Molecular cloning and expression of X. laevis CaMKI-like protein  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 2831)  
AUTHORS Kameshita,I., Kinoshita,S., Sueyoshi,N., Tsuge,T., Suetake,I. and  
Tajima,S.  
TITLE Direct Submission  
JOURNAL Submitted (25-DEC-2002) Isamu Kameshita, Kagawa University,  
Department of Life Sciences; 2393, Ikenobe, Miki-cho, Kita-gun,  
Kagawa 761-0795, Japan (E-mail:kamesita@ag.kagawa-u.ac.jp,  
Tel:81-87-891-3120, Fax:81-87-891-3120)  
FEATURES Location/Qualifiers  
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CDS  
QY 115 TCAAGAAACAGACGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAGCTGGGCTCGG 174  
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Db 152 TCAAGAAGAAATTGAGGACATCAATATGGTGTACAACATCAAGGAGAGCTGGAGCGG 211  
QY 175 GTGCCTTCTCTGAGGTGATGCTGGGCCCAGGAAGGGGCTCTGCTCATCTTGTGGCCCTCA 234  
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Db	212	GGCGTTCTCCGAGTGGTCTTAGCCCAAGAGAAGAAATTCTGAGCGACTGGTGGCCCTGA	271
Qy	235	AGTGCATTCCCAAGAACCACTTCGGGGCAAGGAGGCCCTGGTGGAGAATGAGATCGCGG	294
Db	272	AATGCATCCCTAAGAAAGCTCTCCGAGGGAAAGAGGCCGTGGTAGAGAATGAGATCGCAG	331
Qy	295	TACTTCGAGAAATCAGCCATCCCAACATGTGTGGCTCTGGAGGACGTCCATGAGAGTCCTT	354
Db	332	TGCTGAAGAAGATTACTCACCAAAACATAGTTTCCCTGGACGATATATACGAGAGCCCCA	391
Qy	355	CTCATCTCTACTTGGCCATGGAGCTGGTGAACAGGTGGTGAACCTGTTGACCGCATATGG	414
Db	392	CACACCTGTACTTAGCCATGGAACCTTGTTACTGGAGGGAGCTTTTTCACCGCATCATG	451
Qy	415	AGCGGGCTCTACACAGAGAAGGACGCGCAGCCACCTTGTAGGGCAGGTCCCTTGGCGCTG	474
Db	452	AGCGTGGATATTATACAGAGAAAGATGCCAGTCAACTCATTTGGACAGGTCTCGATGCCG	511
Qy	475	TCTCCTACCTTCATAGCCTGGGCATCGTGCACCGGACCTCAAGCCTGAAAACCTCCTCT	534
Db	512	TACAGTACTTGCACAAACATGGGGATTGTTACCGGAGACCTAAAGCCAGAGAACCTTCTCT	571
Qy	535	ATGCCACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTGGCCTGTCCAAAATAC	594
Db	572	ATGCCACCCCATTTGAGGATTCCAAAATCATGATCAGTGACTTTGGTCTGTCCAAGTTG	631
Qy	595	AAGCTGGCAACATGCTAGGCACAGCCTGTGGGACCCAGGATATGTGGCCCCCAGAGCTCC	654
Db	632	AAGATAGTGAATGATGGCGACAGCGTGGGGACCCCGGATATGTTGCACCAGAACTCC	691
Qy	655	TGGAGCAGAAACCCCTACGGGAAGGCCGTAGATGTGTGGGCCCTGGGTGTCTCTCTACA	714
Db	692	TGGAACAGAGCCGTATGGAAGACTGTAGACGTCTGGCAATTGGTGTCTCTTATA	751
Qy	715	TCCTGCTGTGTGGGTACCCCCCTTCTATGATGAGAGCGATCCCTGAACCTCTTCAGCCAGA	774
Db	752	TTCTGCTCTGCGGTATATCCCCCTTTTACGATGAACGACTCTGAGCTTTTAAACCAGA	811
Qy	775	TTCTGAGGGCCAGCTATGAGTTTGACTCCCCCTTTTGGGATGACATCTCAGAAATCAGCCA	834
Db	812	TCTTGAAGGCAATAACGAATTTGATTCTCCATACTGGGATGACATTTCCGAATCAGCCA	871
Qy	835	AAGACTTCAFTTCGCCACCTTCTGGAACTGATCCCCAGAAAGGTTACCTGCCAGCAGG	894
Db	872	AGGATTTCAATGCTCACTTGTGTGAGAGGGAGCCAGAGAAAAGGCTAAACATGTGAGCAGG	931
Qy	895	CCCTACAGCATCTTTGGATCTCTGGGATGCAGCCTTCGATAGGGACATCCTGGGTTCTG	954
Db	932	CAC'TACAGCATCCCTGGATATGCGGAGACACAGCACTGGAAGAGAGATCCATGGGTCAG	991
Qy	955	TCAGTGACAGATCCAGAAGAAATTTTCCAGGACCCCACTGGAAGCGTGCATTTCAATGCCA	1014
Db	992	TGAGTGAGCAAAATCCAAAGAACTTTTGACCAAGTCACTGGAAGAGAGACTTTCAATGCCA	1051
Qy	1015	CATCATTCCTACGTACATCCGTAAGCTGGGACAAAGCCCCAGAGGGTGAGGA	1066
Db	1052	CTTCGTTCTCCGTACATCACCAAAATGGGGCAAAGTGCTGAGACAGAAGA	1103

RESULT 14  
RATCAMPKAA  
LOCUS RATCAMPKAA 1439 bp mRNA linear ROD 18-MAY-1995  
DEFINITION Rattus norvegicus Cam-like protein kinase mRNA, complete cds.  
ACCESSION L26288  
VERSION L26288.1 GI:439613  
KEYWORDS protein kinase.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
REFERENCE 1 (bases 1 to 1439)  
AUTHORS Cho,F.S., Phillips,K.S., Bogucki,B. and Weaver,T.E.

TITLE	Characterization of a rat cDNA clone encoding calcium/calmodulin-dependent protein kinase I
JOURNAL	Biochim. Biophys. Acta 1224 (1), 156-160 (1994)
MEDLINE	95035115
PUBMED	7948038
COMMENT	Original source text: Rattus norvegicus (strain Sprague-Dawley) (library: day 21 gestation lung cDNA) fetal lung cDNA to mRNA.
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	YDENDAKLFEQILKAEYEFDSPYWDDISDSAKDFIRHLMKEDPEKRTCEQALQHPWI
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ORIGIN	

Query Match	32.9%;	Score 512;	DB 10;	Length 1439;
Best Local Similarity	72.7%;	Pred. No. 2.4e-123;		
Matches 675;	Conservative 0;	Mismatches 250;	Indels 3;	Gaps 1;
QY	119	GAACAGACGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAAAGCTGGGCTCGGGTGC	178	
Db	147	GAAGCAGGACAAGACATTAGGGATATTTATGACTTCAGGGATGTTCTGGGCACGGGTGC	206	
QY	179	CTTCTCTGAGGTGATGCTGGCCCCCAGGAAAGGGGCTCTGCTCATCTTGTGGCCCTCAAGTG	238	
Db	207	CTTCTCAGAAGTGATCCTGGCAGAGGACAAGAGGACTCAGAAACTGGTGGCCATCAAATG	266	
QY	239	CATTCCCAAGAAAGCACTTCGGGGCAAGGAGGCCCTGGTGGAGAATGAGATCGCGGTACT	298	
Db	267	CATTGCCAAGAAAGGCCCTGGAGGGCAAGAAAGGCAGCATGGAGAATGAGATCGCCGTCTT	326	
QY	299	TCGCAGAATCAGCCATCCCAACATTTGTGGCTCTTGAGGACGTCATGAGAGTCCTTCTCA	358	
Db	327	ACACAAGATCAAGCACCCCCAACATTTAGCCCTGGATGACATCTATGAGAGTGGGGGCCA	386	
QY	359	TCTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAACCTGTTTGACCGCATCATGGAGCG	418	
Db	387	CCCTACTCATCATGCAGCTGGTTTCAGGTGGAGAGCTGTTTGACCGAATTTGGAGAA	446	
QY	419	GGGCTCCTACACAGAGAAGGACGCCAGCCACCTTGTAGGGCAGGTCTTGGCGCTGTCTC	478	
Db	447	AGGATTCTACACAGAACGGGATGCCAGCGCCTCATCTTCCAGGTGCTGGATGCTGTCAA	506	
QY	479	CTACCTTCATAGCCTGGGCATCGTGACACCGGGACCTCAAGCCTGAAAACCTCCTCTATGC	538	
Db	507	GTACCTGCACGACCTGGGCATTGTGCACCGGGATCTCAAGCCAGAGAACCTGCTATACTA	566	
QY	539	CACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTTGGCCTGTCCAAAATACAAG-	597	
Db	567	CAGTCTGGATGAAGACTCCAAAATCATGATCTCTGACTTTTGGCCTCTCCAAGATGGAGGA	626	
QY	598	--CTGGCAACATGCTAGGCACAGCCTGTGGGACCCAGGATATGTGGCCCCCAGAGCTCCT	655	
Db	627	CCCAGGCAGTGTGCTCTCCACAGCCTGTGGGACTCCAGGATATGTGGCCCCCTGAGGTCT	686	
QY	656	GGAGCAGAAACCCCTACGGGAAGGCCGTAGATGTGTGGGCCCTGGGTGTCTATCTCCTACAT	715	
Db	687	GGCCCAGAAGCCCTACAGCAAGGCCGTGGACTGCTGGTCCATAGGAGTCATTGCCCTATAT	746	



QY	716	CCTGCTGTGGGTACCC	775
Db	747	ACTGCTCTGTGGCTACCC	806
QY	776	TCTGAGGCCAGCTATGAGTTTGACTCC	835
Db	807	TTTGAAGGCTGAGTATGAGTTTGACTCT	866
QY	836	AGACTTCATTGCCACCTTCTGGAACG	895
Db	867	AGATTTCATACGTCATTTGATGGAGA	926
QY	896	CCTACAGCATCTTTGGATCTCTGGGG	955
Db	927	CTTGACGACCCCTGGATTGCAGGAGAC	986
QY	956	CAGTGAGCAGATCCAGAAGAAATTTTG	1015
Db	987	GAGTGAGCAGATCAAGAAGAACTTTG	1046
QY	1016	ATCATTCCTACGTCACATCCGTAAGCTG	1043
Db	1047	CGCTGTGGTTCGGCACATGAGGAAGCTG	1074

RESULT 15	BC071177	1445 bp	linear	ROD 06-JUL-2004
LOCUS	Rattus norvegicus	regulator of G-protein signalling 19	cdna	(cdna
DEFINITION	clone MGC:91494 IMAGE:7098592)	complete cds.		
ACCESSION	BC071177			
VERSION	BC071177.1	GI:49258137		
KEYWORDS	MGC.			
SOURCE	Rattus norvegicus (Norway rat)			
ORGANISM	Rattus norvegicus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
AUTHORS	1 (bases 1 to 1445)			
	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.			
TITLE	human and mouse cdna sequences	Generation and initial analysis of more than 15,000 full-length		
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)			
PUBMED	12477932			
REFERENCE	2 (bases 1 to 1445)			
AUTHORS	Strausberg,R.			
TITLE	Direct Submission			
JOURNAL	Submitted (24-MAY-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA			
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov			
COMMENT	Contact: MGC help desk			
	Email: cgapbs-r@mail.nih.gov			
	Tissue Procurement: Howard Jacobs			

CDNA Library Preparation: Express Genomics  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),  
Gaithersburg, Maryland;  
Web site: <http://www.nisc.nih.gov/>  
Contact: [nisc\\_mgc@nhgri.nih.gov](mailto:nisc_mgc@nhgri.nih.gov)  
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAX Plate: 175 Row: d Column: 20  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 19745199.

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	/mol_type="mRNA"
	/db_xref="taxon:10116"
	/clone="MGC:91494 IMAGE:7098592"
	/tissue_type="Lung, rat (Brown Norway)"
	/clone_lib="NIH_MGC_231"
	/lab_host="DH10B"
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	/note="synonyms: Gaip, Camki"
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	/db_xref="RGD:629473"
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	/db_xref="GI:49258138"
	/db_xref="LocusID:171503"
	/db_xref="RGD:629473"
	/translation="MPGAVEGPRWQAEIRDIVFRDLVLTGAFSEVILAEDKRTQK LVAIKCIAKALEGKESMENEI AVLHKIPNIVALDDIYESGGHLYLIMQLVSGGE LFDRIVEKGFYTERDASRLIFQVLDAVKYLDLGLIVHRDLKPENLLYSLDEDSKIMI SDFGLSKMEDPGSVLSTACGTPGYVAPEVLAQKPYSAVDKWSIGVIAYILLCGYPPE YDENDAKLFEQILKAEYEFDSPYWDDISDSAKDFIRHLMKDPKFRFTCEQALQHPWI AGDTALDKNIHQSVSEQIKKNFAKSKWQAFNATAVVRMRKQLQGTSEQGQGTASH GELLTPTAGGPAAGCCCRDCCVEPSELPPAPPSSRAM"
ORIGIN	
	Query Match 32.9%; Score 512; DB 10; Length 1445;
	Best Local Similarity 72.7%; Pred. No. 2.4e-123;
	Matches 675; Conservative 0; Mismatches 250; Indels 3; Gaps 1;
QY	119 GAAACAGACGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAGCTGGGCTCGGGTGC 178
Db	82 GAAGCAGGCAGAAAGACATTAGGGATATTATGACTTCAGGGATGTTCTGGGCACGGGTGC 141
QY	179 CTTCTCTCAGGTGATGCTGGCCAGGAAAGGGGCTCTGCTCATCTTGTGGCCCTCAAGTG 238
Db	142 CTTCTCAGAAAGTGATCCTGGCAGAGGACAAGAGGACTCAGAAACTGTTGGCCATCAAATG 201
QY	239 CATTCCCAAGAAAGCACTTCGGGGCAAGAGGCCCTGGTGGAGATGAGATCGCGGTACT 298
Db	202 CATTGCCAAGAAGGCCCTGGAGGSCAAAGAGGCAGCATGGAGATGAGATCGCGGTCTT 261
QY	299 TCGCAGATCAGCCATCCCAACATTGTGGCTCTGGAGGACGTCCTCATGAGAGTCTTCTCA 358
Db	262 ACACAAGATCAAGCACCCCAACATTGTAGCCCTGGATGACATCTATGAGAGTGGGGCCA 321

Qy	359	TCTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAACCTGTTGACCCGCATCATGGAGCG	418
Db	322	CCTCTACCTCATCATGCAGCTGGTTTCAGGTGGAGAGCTGTTGACCGAATTGTGGAGAA	381
Qy	419	GGGCTCCTACACAGAGAAAGGACGCCAGCCACCTTGTAGGGCAGGTCCCTTGGCGCTGTC	478
Db	382	AGGATTCTACACAGAACGGGATGCCAGCCGCCTCATCTTCCAGGTGCTGGATGCTGTCAA	441
Qy	479	CTACCTTCATAGCCTGGGCATCGTGACCCGGGACCTCAAGCCTGAATAACCTCCTCTATGC	538
Db	442	GTACCTGCACGACCTGGGCAATTGTGCACCGGGATCTCAAGCCAGAGAACCTGCTATACTA	501
Qy	539	CACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTGGCCTGTCCAAAATACAAG-	597
Db	502	CAGTCTGGATGAAGACTCCAAAATCATGATCTCTGACTTTGGCCTCTCCAAGATGGAGGA	561
Qy	598	--CTGGCAACATGCTAGGCACAGCCTGTGGGACCCCGAGGATATGTGGCCCGCAGAGCTCCT	655
Db	562	CCCAGGCAGTGTGCTCTCCACAGCCTGTGGGACTCCAGGATATGTGGCCCTGAGGTCCT	621
Qy	656	GGAGCAGAAACCCCTACGGGAAGGCCGTAGATGTGTGGGCCCTGGGTGTCTATCTCCTACAT	715
Db	622	GGCCCAAGACCCCTACAGCAAGGCCGTGGACTGCTGGTCCATAGGAGTCATTGCCTATAT	681
Qy	716	CCTGCTGTGGGTACCCCCCTTCTATGATGAGAGCGATCCTGAACTCTTTCAGCCAGAT	775
Db	682	ACTGCTCTGTGGCTACCCGCCGTTCTATGATGAAAAATGATGCCAAACTTTTGAACAGAT	741
Qy	776	TCTGAGGCGCAGCTATGAGTTTGACTCCCCCTTTTGGGATGACATCTCAGAATCAGCCAA	835
Db	742	TTTGAAGGCTGAGTATGAGTTTGACTCTCCTTATTTGGACGACATCTCTGACTCTGCCAA	801
Qy	836	AGACTTCATTGCGCCACCTTCTGGAACGTGATCCCCAGAGAGGTTTCACCTGCCAGCAGGC	895
Db	802	AGATTTCATACGTCAATTGTGATGGAGAAAGACCCAGAGAGAGGTTTCACCTGTGAGCAGGC	861
Qy	896	CCTACAGCATCTTTGGATCTCTGGGGATGCGAGCCTTCGATAGGGACATCCTGGGTTCTGT	955
Db	862	CTTGCAGCACCCCTGGATTGCAGGAGACACAGCTCTGGATAAGATATCCACCAGTCAGT	921
Qy	956	CAGTGAGCAGATCCAGAAAGAAATTTTGGCAGGACCCACTGGAAGCGGTGCAATTCAATGCCAC	1015
Db	922	GAGTGAGCAGATCAAGAAAGAACTTTGCCAAGAGCAAGTGGAGCAAGCTTTCAATGCTAC	981
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Search completed: June 6, 2005, 03:37:34  
Job time : 10897 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 5, 2005, 22:38:35 ; Search time 1266 Seconds  
(without alignments)  
7266.412 Million cell updates/sec

Title: US-10-032-254A-1  
Perfect score: 1554  
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Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues  
Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1261.2	81.2	1458	2 AAV18867	AAV18867 Calmoduli
2	859	55.3	1584	12 ADM43841	Adm43841 Novel hum
3	844.4	54.3	1282	2 AAX06835	Aax06835 Disease a
4	844.4	54.3	1282	10 ACA56355	ACA56355 Norway ra
5	844.4	54.3	1282	12 ADI56151	Adi56151 Human pol
6	844.4	54.3	1282	12 ADL06429	Adl06429 Human tum
7	844.4	54.3	1282	12 ADM72654	Adm72654 Human TAS
8	844.4	54.3	1282	12 ADM72236	Adm72236 Human TAS
9	836.8	53.8	1032	4 AAS06711	Aas06711 Polynucle
10	803.6	51.7	1216	6 ABZ11323	Abz11323 Human pol
11	800.2	51.5	1180	13 ADR39798	Adr39798 Human kin
12	699	45.0	1656	8 ACC46211	Acc46211 Human dit
13	681.8	43.9	1371	8 ACC46241	Acc46241 Human dit
14	671.6	43.2	1646	12 ADE28342	Ade28342 Human KPP
15	588.8	37.9	1120	12 ADI40898	Adi40898 Human kin
16	544	35.0	641	12 ADM72664	Adm72664 Human TAS
17	512	32.9	1439	10 ADB53683	Adb53683 Primary r
18	502.4	32.3	1402	10 ADB57940	Adb57940 Toxicity-
19	500.8	32.2	1480	8 AAD52784	Aad52784 Human cam
20	500.8	32.2	1480	10 ACA56856	Aca56856 Human sig

21	500.8	32.2	1480	12 ADI56652	Adi56652 Human pol
22	500.8	32.2	1501	12 ADL97819	Adl97819 Human typ
23	500.8	32.2	1501	13 ADP23703	Adp23703 PRO polyp
24	447.6	28.8	1197	12 ADI40938	Adi40938 Human kin
25	437.8	28.2	1736	4 AAD18817	Aad18817 Human kin
26	436.2	28.1	1074	4 AAS06708	Aas06708 Polynucle
27	436.2	28.1	1074	4 AAH25119	AAh25119 Nucleotid
28	436.2	28.1	1158	4 AAH25118	AAh25118 Nucleotid
29	436.2	28.1	1565	6 ABL60905	ABl60905 Human Cam
30	436.2	28.1	1578	4 AAD04775	Aad04775 Human dea
31	436.2	28.1	1579	12 ADJ74939	Adj74939 Marker ge
32	436.2	28.1	1579	12 ADQ15043	Adq15043 Human can
33	436.2	28.1	1661	4 AAD18826	Aad18826 Human kin
34	436.2	28.1	1671	4 AAH25120	AAh25120 Nucleotid
35	436.2	28.1	1733	4 AAI58638	Aai58638 Human pol
36	436.2	28.1	1733	5 ADQ98856	Adq98856 DNA encod
37	436.2	28.1	1733	9 ADB48616	ADB48616 Novel hum
38	436.2	28.1	2164	4 AAI60424	Aai60424 Human pol
39	431.2	27.7	709	4 ABK43538	Abk43538 DNA encod
40	431.2	27.7	709	12 ADI53925	Adi53925 cDNA enco
41	430	27.7	1383	6 ABK99973	Abk99973 Human CAD
42	430	27.7	1738	6 ABK99974	Abk99974 Human CAD
43	430	27.7	1956	4 AAI60703	Aai60703 Human pol
44	428.4	27.6	2447	6 AAD36140	Aad36140 Human cal
45	428.2	27.6	1694	4 AAC90432	Aac90432 Murine De

ALIGNMENTS

RESULT 1  
AAV18867  
ID AAV18867 standard; cDNA; 1458 BP.  
XX  
AC AAV18867;  
XX  
DT 09-JUL-1998 (first entry)  
XX  
DE Calmodulin-dependent protein kinase clone 29 cDNA.  
XX  
KW Rat; calmodulin-dependent protein kinase; clone 29; ds.  
XX  
OS Rattus rattus.  
XX  
FH Key Location/Qualifiers  
FT CDS 50..1125  
FT /\*tag= a  
FT /product= "calmodulin-dependent\_protein\_kinase"  
FT /transl\_except= (pos:1079..1080, aa:Val)  
FT /note= "this codon has an apparent 1 nucleotide deletion,  
FT that alters the reading frame"

WO9805352-A1.

12-FEB-1998.

01-AUG-1997; 97WO-US013657.

02-AUG-1996; 96US-0023220P.

(SCRI ) SCRIPPS RES INST.

Sutcliffe JG, Gautvik KM, De Lecea L, Bloom FE, Danielson PE;

Gautvik VT, Kilduff TS, Foye PE;

WPI; 1998-145352/13.

P-PSDB; AAW50159.

Nucleic acid encoding hypocretin of rat and mouse - useful for diagnosis and treatment of neurological disease, homeostatic dysfunction etc., also sequence for calmodulin kinase-like protein.

Claim 55; Fig 6; 111pp; English.



```
XX The present sequence encodes rat calmodulin-dependent protein kinase
CC clone 29
XX
SQ Sequence 1458 BP; 311 A; 406 C; 403 G; 338 T; 0 U; 0 Other;
  Query Match      81.2%; Score 1261.2; DB 2; Length 1458;
  Best Local Similarity 93.6%; Pred. No. 0;
  Matches 1348; Conservative 0; Mismatches 63; Indels 29; Gaps 2;
QY 99 GCAGACATGCTGCTGCTCAAGAAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGG 158
Db 44 GCAGACATGCTGCTGCTCAAGAAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGG 103
QY 159 GAGAAGCTGGGCTCGGTGCCCTTCTCTGAGGTGATGCTGGCCAGGAAAGGGCTCTGCT 218
Db 104 GAGAAGCTGGGCTCGGTGCCCTTCTCTGAGGTGATGCTGGCCAGGAAAGGGCTCTGCT 163
QY 219 CATCTTGTGGCCCTCAAGTGCAATCCCAAGAAAGCACTTCGGGGCAAGGAGGCCCTGGTG 278
Db 164 CATCTTGTGGCCCTCAAGTGCAATCCCAAGAAAGCACTTCGGGGCAAGGAGGCCCTGGTG 223
QY 279 GAGAATGAGATCGCGGTACTTCGCAGAAATCAGCCATCCCAACATTGTGGCTCTGGAGGAC 338
Db 224 GAGAATGAGATCGCAGTACTCCGAGGATTAGCCACCCCAACATTGTGGCTCTGGAGGAC 283
QY 339 GTCCATGAGATGCTTCTCATCTCTACTTTGGCCATGGAGCTGGTAACAGGTGGTGAAC TG 398
Db 284 GTCCACGAGAGCCCTTCCCATCTCTACTTTGGCCATGGAGCTGGTAACAGGTGGTGAAC TG 343
QY 399 TTTGACCGCATCATGGAGCGGGCTCTTACACAGAGAAGGACGCCAGCCACTTGTAGGG 458
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Db 404 CAGGTCTTGGTGTGTCTCTACCTTCATAGCCTGGGCATCGTGCAACCGGACCTCAAG 463
QY 519 CCTGAAACCTCTCTATGCCACACCTTTTGGAGACTCCAAGATCATGGTCTCTGACTTT 578
Db 464 CCTGAAACCTCTCTATGCCACACCTTTTGGAGACTCCAAGATCATGGTCTCTGACTTT 523
QY 579 GGCCTGTCCAAATACAAAGCTGGCAACATGTAGGCACAGCCTGTGGACCCCCAGGATAT 638
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Db 584 GTGGCCCCAGAGCTCTGGAGCAGAAACCCCTACGGGAAGGCCGTAGATGTGTGGCCCTG 643
QY 699 GGTGTCACTCTCTACATCTCTGTGTGGGTACCCCCCTTCTATGATGAGAGCGATCCT 758
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Db 704 GAACTCTTCAGCCAGATTCTGAGGGCCAGCTACGAGTTTGACTCTCCCTTTTGGGATGAC 763
QY 819 ATCTCAGAATCAGCCAAAGACTTTCATTTCGCCACCTTCTGGAACGTGATCCCCAGAAAGG 878
Db 764 ATCTCAGAATCAGCCAAAGACTTTCATTTCGCCACCTTCTGGAACGTGATCCCCAGAAAGG 823
QY 879 TTCACCTGCCAGCGGCCCTTACAGCATCTTTGGATCTCTGGGGATGCAGCCTTCGATAGG 938
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QY 939 GACATCCTGGGTTCTGTCAGTGAGCAGATCCAGAGAATTTTCCAGGACCCACTGGAAG 998
Db 884 GACATCCTAGGTTCTGTCAGTGAGCAGATCCAGAGAATTTTCCAGGACCCACTGGAAG 943
QY 999 CGTGCAATCAATGCCACATCATCTCTACGTTCACATCCGTAAGCTGGGACAAAGCCCAGAG 1058
Db 944 CGTGCAATCAATGCCACATCATCTCTACGTTCACATCCGTAAGCTGGGACAGAGCCCAGAG 1003
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Db 1064 CAGTCTCCCAAGTGGTGACAACACAGGTGGATGCCAAGGAAGGCCAAGTGACTGACTCCT 1123
QY 1179 GGTTTTCTTTTCTCCTCCAGCCCTTTTGGTCTCTTTTCTGGATCCTTCTCCTCCAGACTGGC 1238
Db 1124 AGCTTTTCTTTCTCCTCCAGCCCTTTGATCTCCTTCCCTGATCCTTGTCCCCGGACTGGC 1183
QY 1239 CTCTGCTGGAAGTCTGAGAC--TGGGTGTGATGCATGGCATAAGGTACGGGTACGGGCTTCCC 1296
Db 1184 CTCTGTGGAAGTCCAAGACCGTGGGTGTGATGCATGGCATAAGGTATGGGGCTTCCC 1243
QY 1297 CAGTATGTCCCCCAGCCCTCTATTCTTACCTATGGTGGAGGCTCCCTTCCCCTATGTGCTG 1356
Db 1244 AAGTATGTCCCC-----AGCCTCTGTCTCTTGTGCTG 1276
QY 1357 CCACCTCTATGGAAACTGAGGAGTGTTCAAAAGTGGACTTTGGGAGCCATCCTTCTCTGC 1416
Db 1277 CCACCTCTATGGAAACTGAGGAGTATTCAAAAATGGATTGGGGCCATCCTTCTCTGC 1336
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Db 1337 ACCTTGACAGCACATATGCATTGCGTGGTGTCTGTGCTTTGCTGACTGTGGGTGGTCC 1396
QY 1477 TGCTTGTGTGTGGCCCTTTAGTTTCTCTCTCTTTTCTTAACCAATAAAGACAAACAGAACCA 1536
Db 1397 TGCTTGTGTGTAGCCCTTTAGTTTCTCTCTCTTTTCCAACCAATAAAGACAAACAGAACCA 1456
RESULT 2
ADMA3841
ID ADM43841 standard; cDNA; 1584 BP.
XX
AC ADM43841;
XX
DT 03-JUN-2004 (first entry)
XX
DE Novel human arginine-rich protein cDNA #205.
XX
KW ss; gene; human; arginine-rich protein; cancer; inflammation;
  genetic disorder.
XX
OS Homo sapiens.
XX
PN US2004053250-A1.
PD 18-MAR-2004.
XX
PF 21-NOV-2002; 2002US-00302172.
XX
PR 05-MAR-2001; 2001US-00799451.
PR 05-MAR-2002; 2002WO-US005095.
PR 20-AUG-2002; 2002US-00225251.
XX
PA (TANG/) TANG Y T.
PA (XUEA/) XUE A.
PA (DRMA/) DRMANAC R T.
XX
PI Tang YT, Xue A, Drmanac RT;
XX
DR WPI; 2004-238579/22.
XX
PT New isolated arginine-rich protein-like polynucleotides and polypeptides,
  useful for diagnosing and/or treating conditions associated with aberrant
  activity of the arginine-rich polypeptides, such as cancer and
  inflammation.
XX
PS Disclosure; SEQ ID NO 205; 51pp; English.
```

The invention relates to an isolated polynucleotide. The methods and compositions of the present invention are useful for the diagnosis and/or treatment of diseases or conditions associated with aberrant expression or activity of the arginine-rich protein-like polypeptides, such as cancer and inflammation. They can also be used in forensics, gene mapping, identification of mutations responsible for genetic disorders, and in assessing biodiversity. The present sequence represents a novel human arginine-rich protein cDNA.

SQ    Sequence 1584 BP; 282 A; 530 C; 457 G; 315 T; 0 U; 0 Other;  
       Query Match            55.3%;    Score 859;    DB 12;    Length 1584;  
       Best Local Similarity    78.7%;    Pred. NO. 4.3e-216;  
       Matches 1098;    Conservative    0;    Mismatches 270;    Indels 27;    Gaps 5;

QY	168	GGCTCGGGTGCTTCTCTGAGGTGATGCTGGCCCAAGAAAGGGGCTCTGCTCATCTGTG	227
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QY	228	GCCCTCAAGTGCAATCCCAAGAAAGCACCTCGGGCAAGAGGCCCTGGTGGAGAATGAG	287
Db	261	GCCCTCAAGTGCAATCCCAAGAGGCCCTCCGGGCAAGAGGCCCTGGTGGAGAACGAG	320
QY	288	ATCGCGGTACTTCGCAGAAATCAGCCATCCCCAACATTTGTGGCTCTGGAGGACGTCCATGAG	347
Db	321	ATCGCAGTGCTCCGTAGGATCAGTACCCCCAACATCTGTCGCTCTGGAGGATGTCCACGAG	380
QY	348	AGTCCTTCTCATCTCTACTTTGGCCATGGAGCTGGTAACAGGTGGTGAACTGTTTGACCGC	407
Db	381	AGCCCTTCCCACCTTACCTGGCCATGGAACTGGTGACGGGTGGCGAGCTGTTTGACCGC	440
QY	408	ATCATGGAGCGGGGTCTCTACACAGAGAAGGACGCCAGCCACCTTGTAGGGCAGGTCTT	467
Db	441	ATCATGGAGCGGGTCTCTACACAGAGAAGGATGCCAGCCATCTGGTGGGTCAAGTCTT	500
QY	468	GGCGCTGTCTCTTACCTTCTATAGCCTGGGCATCGTGACCCGGGACCTCAAGCCTGAAAAC	527
Db	501	GGCGCGTCTCTTACCTGCACAGCCTGGGGATCGTGACCCGGGACCTCAAGCCCGAAAAC	560
QY	528	CTCCTCTATGCCACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTGGCCCTGTCC	587
Db	561	CTCCTGTATGCCACGCGCTTTGAGGACTCGAAGATCATGGTCTCTGACTTTGGACTCTCC	620
QY	588	AAAATACAAGCTGGCAACATGCTAGGCACAGCCTGTGGGACCCAGGATATGTGGCCCCA	647
Db	621	AAAATCCAGGCTGGAAACATGCTAGGCACCGCCTGTGGACCCCTGGATATGTGGCCCCA	680
QY	648	GAGCTCCTGGAGCAGAAAACCTTACGGGAAGGCCGTAGATGTGTGGCCCTGGGTGTGATC	707
Db	681	GAGCTCTTGGAGCAGAAAACCTTACGGGAAGGCCGTAGATGTGTGGCCCTGGGTGTGATC	740
QY	708	TCCTACATCCTGTGTGTGGGTACCCCCCTTCTATGATGAGAGCGATCCTGAACTCTTC	767
Db	741	TCCTACATCCTGTGTGTGGGTACCCCCCTTCTACGACGAGAGCGACCTGAGCTCTTC	800
QY	768	AGCCAGATTCTGAGGCCAGCTATGAGTTTGACTCTCTGATGAGAGCGATCCTCAGAA	827
Db	801	AGCCAGATCCTGAGGCCAGCTATGAGTTTGACTCTCTGATGAGATGACATCTCAGAA	860
QY	828	TCAGCCAAAGACTTCATTGCGCCACCTTCTGGAAACGTGATCCCCAGAAAGAGTTTCACTGC	887
Db	861	TCAGCCAAAGACTTCATCCGGCACCTTCTGGAGCGAGACCCCGAAGAGGTTTCACTGC	920
QY	888	CAGCAGGCCCTACAGCATCTTTGGATCTCTGSSGATGCAGCCCTTCGATAGGGACATCCTG	947
Db	921	CAACAGGCCCTTGCAGCACCTTTGGATCTCTGGGGACACAGCCTTCGACAGGGACATCTTA	980
QY	948	GGTTCTGTAGTGACAGATCCAGAAAGAAATTTTGCAGGACCCACTGGAAGCGTGCAATTC	1007
Db	981	GGCTCTGTAGTGAGCAGATCCGGAAGAACTTTGCTCGGACACACTGGAAGCGAGCCTTC	1040
QY	1008	AATGCCACATCATCTCTACGTCAATCCGTAAGCTGGGACAAAAGCCAGAGGGTGAAGAG	1067







PF 26-NOV-2002; 2002US-00305720.  
XX  
PR 30-JAN-1998; 98US-00016434.  
XX  
PA (INCY-) INCYTE GENOMICS INC.  
XX  
PI Au-Young J, Seilhamer JJ;  
XX  
DR WPI; 2004-090520/09.  
XX  
XX  
PT New composition comprising polynucleotide probes, useful as array  
PT elements in a microarray for monitoring the expression of target  
PT polynucleotides or purifying a subpopulation of mRNAs, cDNA, or genomic  
PT fragments.  
XX  
PS Claim 6; SEQ ID NO 953; 73pp; English.  
XX  
CC The invention relates to a composition of polynucleotide probes  
CC comprising first polynucleotide probes comprising at least a portion of a  
CC gene encoding a receptor-like polypeptide, second polynucleotide probes  
CC comprising at least a portion of a gene encoding a transducing  
CC polypeptide and third polynucleotide probes comprising at least a portion  
CC of a gene encoding an effector-like polypeptide. The probes of the  
CC composition are useful as array elements in a microarray for monitoring  
CC the expression of target polynucleotides. The microarray is useful in the  
CC diagnosis and treatment of cancer, an immunopathology or a  
CC neuropathology. It can also be used for drug discovery and development,  
CC toxicological and carcinogenicity studies, forensics or pharmacogenomics.  
CC Microarrays can also be used for monitoring the progression of diseases  
CC that may be associated with the altered expression of signalling pathway  
CC polypeptides. The composition can also be used to purify a subpopulation  
CC of mRNAs, cDNAs, or genomic fragments in a sample. The expression profile  
CC is also useful for the diagnosis and treatment of cancer, e.g. cancers of  
CC the adrenal gland, bladder, bone, bone marrow, brain, breast or cervix,  
CC an immunopathology, e.g. AIDS, diabetes, pancreatitis, osteoporosis or  
CC ulcerative colitis, or a neuropathology, e.g. dementia, amnesia,  
CC epilepsy, Alzheimer's disease or depression. This sequence represents a  
CC human polynucleotide probe of the invention. Note: The sequence data for  
CC this patent did not form part of the printed specification but was  
CC obtained in electronic format directly from USPTO at  
XX seqdata.uspto.gov/sequence.html.  
SQ Sequence 1282 BP; 275 A; 370 C; 383 G; 245 T; 0 U; 9 Other;  
Query Match 54.3%; Score 844.4; DB 12; Length 1282;  
Best Local Similarity 86.2%; Pred. No. 2.8e-212;  
Matches 940; Conservative 1; Mismatches 145; Indels 4; Gaps 1;  
QY 101 AGACATGCTGCTCAAGAAACAGACGGAGACATCAGCAGTGTCTATGAGATCCGGGA 160  
DB 197 AAACATGCTGCTGAAGAAACACACGGAGGACATCAGCAGCGTCTACGAGATCCGCGA 256  
QY 161 GAAGCTGGGCTCGGTGCCTTCTCTGAGGTGATGCTGGCCAGGAAAGGGGCTCTGTCA 220  
DB 257 GAGGCTCGGCTCGGTGCCTTCTCCGAGGTGGTGTGCTGGCCAGGAGCGGGGCTCCGCACA 316  
QY 221 TCTTGTGGCCCTCAAGTGCATTCCCAAGAAAGCACTTCGGGGCAAGAGGCCCTGGTGA 280  
DB 317 CCTGTGGCCCTCAAGTGCATCCCCAAGAGGCCCTCCGGGGCAAGAGGCCCTGGTGA 376  
QY 281 GAATGAGATCGCGGTACTTCGCAGAAATCAGCATCCCCAACATTGTGGCTCTGGAGGACGT 340  
DB 377 GAACGAGATCGCAGTGTCCGTAGGATCAGTACCCCCAACATCGTCGCTCTGGAGGATGT 436  
QY 341 CCATGAGAGTCTTCTCATCTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAACCTGTT 400  
DB 437 CCACGAGAGCCCTTCCACCTCTACCTGGCCATGGAACTGGTGACGGGTGGCGAGCTGTT 496  
QY 401 TGACCGCATCATGGAGCGGGGCTCCTACACAGAGAAGGACGCCAGCCACCTGTAGGGCA 460  
DB 497 TGACCGCATCATGGAGCGGGGCTCCTACACAGAGAAGGATGCCAGCCATCTGGTGGGTCA 556  
QY 461 GGTCTTGGCGCTGTCTCCTACCTTTCATAGCCTGGGCATCGTGCACCGGGACCTCAAGCC 520

Db 557 GGTCCTTGGCGCGCTCTCCTACTGCACAGCCTGGGGATCGTGACCGGGACCTCAAGCC 616  
QY 521 TGAAAACTCTCTATGCCACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTGG 580  
Db 617 CGAAAACTCTCTGTATGCCACGCGCTTTGAGGACTCGAAGATCATGGTCTCTGACTTTGG 676  
QY 581 CCTGTCCAAAAATACAAGCTGGCAACATGCTAGGCACAGCCTGTGGACCCCCAGGATATGT 640  
Db 677 ACTCTCCAAAAATCCAGGCTGGGAACATGCTAGGCACCGCCTGTGGACCCCTGGATATGT 736  
QY 641 GGCCCCAGAGCTCTCTGGAGCAGAAACCCCTACGGGAAGGCCGTAGATGTGTGGCCCTGGG 700  
Db 737 GGCCCCAGAGCTCTTGGAGCAGAAACCCCTACGGGAAGGCCGTAGATGTGTGGCCCTGGG 796  
QY 701 TGTATCTCTACATCCTGCTGTGTGGGTACCCCCCTTCTATGATGAGAGCGATCCTGA 760  
Db 797 CGTCACTCTCTACATCCTGCTGTGTGGGTACCCCCCTTCTACGACGAGAGCGACCTGA 856  
QY 761 ACTCTTCAGCCAGATTCTGAGGGCCAGCTATGAGTTTGACTCCCCCTTTTGGGATGACAT 820  
Db 857 GCTCTTCAGCCAGATCCTGAGGGCCAGCTATGAGTTTGACTNTCCTTCTTGGGATGACAT 916  
QY 821 CTCAGAATCAGCCAAAGACTTCAATTCGCCACCTTCTTGGAACTGATCCCCAGAAAGAGTT 880  
Db 917 CTCAGAATCAGGCAAGACTTTATTTCGGCACCTTCTTGAGCGGAGACCTTCAGAAGAGGTT 976  
QY 881 CACCTGCAGCAGGCCCTTACAGCATCTTTGGATCTCTGGGATGCAGCCTTCGATAGGGA 940  
Db 977 CACCTGCCAACAGGCCCTTCGGGGACCTTTGGATCTTTTGGACACAGGCTTTGGCAGGGA 1036  
QY 941 CATCCTGGGTTCTGTCACTGAGCAGATCCAGAAGAAATTTTGCAGGACCCACTGGAAGCG 1000  
Db 1037 CATCTTAGGGTTTGTCACTGAGCAGATCCGGAAGAACTTTTGTGGACACACTGGAAGCG 1096  
QY 1001 TGCATTCAATGCCACATCATTTCTTACGTACATCCGTAAGCTGGGACAAAGCCCAGAGGG 1060  
Db 1097 AGCCTTCAATGCCACCTTGTTCCTGCGCCACATCCGGAAGCTGGGGCAGATCCCAGAGGG 1156  
QY 1061 TGAGGAGGCTCCAGGCAGTGTATGACCCGTATAGCCACCCAGGCTTGGGACTAGCCA 1120  
Db 1157 CGAGGGGGCTCTGAGCAGGGCATGGSCCGNCACAGCCACTNAGGCCTTCGTGCTGGCCA 1216  
QY 1121 GTCCCCCAAGTGGTGAACACCAGGTAGATGCCAAGGAAGGCCAAGTGGACTGACTCCCGG 1180  
Db 1217 GCCCCCCAAGTGGTGTATGCCCAGGNAGATGCC---GAGGCCAAGTGGANTGANCCCCAG 1272  
QY 1181 TTTTTCCTTC 1190  
Db 1273 ATTNCTTNC 1282  
RESULT 6  
ADL06429  
ID ADL06429 standard; cDNA; 1282 BP.  
XX  
AC ADL06429;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Human tumour-associated antigenic target (TAT) cDNA sequence #9.  
XX  
KW Human; tumour-associated antigenic target; TAT; cell death; tumour;  
KW cancer; cytostatic; gene; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO2004016225-A2.  
XX  
PD 26-FEB-2004.  
XX  
PF 19-AUG-2003; 2003WO-US025892.  
XX







XX Claim 2; SEQ ID NO 41; 163pp; English.

XX The invention relates to new isolated tumour-associated kinase (TASK)

CC nucleic acid molecules and encoded polypeptides. Cytostatic. The

CC antibody, oligopeptide or organic molecule that binds to the TASK

CC polypeptide are useful for treating a mammal having a tumour comprising

CC cells expressing the polypeptide. Antagonists of TASK are useful for

CC treating or preventing a cell proliferative disorder (e.g. cancer)

CC associated with increased expression or activity of TASK polypeptide. The

CC TASK polynucleotides and polypeptides may be used as hybridization probes

CC for isolating full length TASK DNA, for generating transgenic animals, in

CC chromosome identification, or for tissue typing. The present sequence

CC represents a cDNA encoding a human TASK polypeptide.

XX

SQ Sequence 1282 BP; 275 A; 370 C; 383 G; 245 T; 0 U; 9 Other;

Query Match 54.3%; Score 844.4; DB 12; Length 1282;

Best Local Similarity 86.2%; Pred. No. 2.8e-212;

Matches 940; Conservative 1; Mismatches 145; Indels 4; Gaps 1;

QY 101 AGACATGCTGCTCAAGAAAACAGACGAGGACATCAGCAGTGTCTATGAGATCCGGGA 160

DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

DB 197 AAACATGCTGCTGAAGAAAACACACGAGGACATCAGCAGCTCTACGAGATCCGCGA 256

QY 161 GAAGCTGGGCTCGGGTGCCTTCTCTGAGGTGATGTGGCCCCAGGAAAGGGGCTCTGCTCA 220

DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

DB 257 GAGGCTCGGCTCGGTGCTTCTCGAGGTGGTGGTGGCCCCAGGAGCGGGGCTCCGCACA 316

QY 221 TCTTGTGGCCCTCAAGTGCATTCCCAAGAAAGCACTTCGGGGCAAGGAGGCCCTGGTGA 280

DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

DB 317 CCTCGTGGCCCTCAAGTGCATCCCAAGAGGCCCTCCGGGGCAAGGAGGCCCTGGTGA 376

QY 281 GAATGAGATCGCGTACTTTCGAGAATCAGCCATCCCAACATTGTGGCTCTGGAGGACGT 340

DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

DB 377 GAACGAGATCGCAGTGTCTCGTAGGATCAGTACGCCCAACATCGTCGCTCTGGAGGATGT 436

QY 341 CCATGAGAGTCTTCTCATCTCTACTTGGCCATGAGCTGGTAACAGGTGGTGAAGTGT 400

DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

DB 437 CCACGAGAGCCCTTCCACCTCTACCTGGCCATGGAAGTGGTACGGGTGGCGAGCTGT 496

QY 401 TGACCGCATCATGAGCGGGGCTCCTACACAGAGAAGGACGCCAGCCACCTTGTAGGGCA 460

DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

DB 497 TGACCGCATCATGAGCGGGGCTCCTACACAGAGAAGGATGCCAGCCATCTGGTGGTCA 556

QY 461 GGTCTTGGCGCTGTCTCCTACCTTACATAGCCCTGGGCATCGTGACCCGGGACCTCAAGCC 520

DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

DB 557 GGTCTTGGCGCGTCTCCTACCTGACAGCCCTGGGGATCGTGACCCGGGACCTCAAGCC 616

QY 521 TGAACACCTCCTATGCCCACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTGG 580

DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

DB 617 CGAAACCTCCTGTATGCCACGCCCTTTGAGGACTCGAAGATCATGGTCTCTGACTTTGG 676

QY 581 CCTGTCCAAATAACAAGCTGGCAACATGCTAGGCACAGCCCTGTGGACCCCGAGGATATGT 640

DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

DB 677 ACTCTCCAAATCCAGGCTGGGAACATGCTAGSCACCGCCTGTGGACCCCTGGATATGT 736

QY 641 GGCCCCAGAGCTCCTGGAGCAGAAACCCCTACGGGAAGGCCGTAGATGTGTGGCCCTGGG 700

DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

DB 737 GGCCCCAGAGCTCTGGAGCAGAAACCCCTACGGGAAGGCCGTAGATGTGTGGCCCTGGG 796

QY 701 TGTATCTCCTACATCCTGTGTGGGTACCCCCCTTCTATGATGAGAGCGATCCTGA 760

DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

DB 797 CGTCATCTCCTACATCCTGTGTGGGTACCCCCCTTCTACGACGAGAGGACCCCTGA 856

QY 761 ACTCTTCAGCCAGATCTTGAGGGCCAGCTATGAGTTTGACTCCCCCTTTTGGGATGACAT 820

DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

DB 857 GCTCTTCAGCCAGATCCTGAGGGCCAGCTATGAGTTTGACTNTCCTTCTCTGGATGACAT 916

QY 821 CTCAGAATCAGCCAAAGACTTCATTCCGCCACCTTCTGGAACGTGATCCCCAGAGAGGTT 880

DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

DB 917 CTCAGAATCAGGCAAGACTTTATTTCGGCACCTTCTGGAGCGAGACCTTCAGAAGAGGTT 976

QY 881 CACCTGCCAGAGCCCTACAGCATCTTTGGATCTCTGGGATGCAGCCCTTCGATAGGGA 940

DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

DB 977 CACCTGCCAACAGGCTTGGGGACCTTTGGATCTTTTGGACACAGGCTTTGGCAGGGA 1036

QY 941 CATCTGGGTTCTGTCAAGTGCAGATCCAGAGAATTTTGCAGGACCCACTGGAAGCG 1000

DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

DB 1037 CATCTTAGGTTTGTCAAGTGCAGATCCGGAAGAACTTTGCTTGGACACACTGGAAGCG 1096

QY 1001 TGCATTCAATGCCACATCATTCTACGTACATCCGTAAGCTGGGACAAAGCCAGAGGG 1060

DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

DB 1097 AGCCTTCAATGCCACCTTGTCTCGGCCACATCCGGAAGCTGGGCGAGATCCAGAGGG 1156

QY 1061 TGAGGAGGCCCTCCAGGCAGTGTATGACCCGTATAGCCACCCAGGCCCTTGGGACTAGCCA 1120

DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

DB 1157 CGAGGGGGCTCTGAGCAGGGCATGSSCCGNCACAGCCACTNAGGCCCTTCGTGCTGGCCA 1216

QY 1121 GTCCCCCAAGTGTGAAACCAGGTAGATGCCAAGGAAGCCAAAGTGGACTGACTCCCGG 1180

DB | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

DB 1217 GCCCCCAAGTGTGATGATGCCAGGNAGATGCC----GAGGCCAAGTGGANTGANCCTCAG 1272

QY 1181 TTTTCTTTTC 1190

DB | | | | |

DB 1273 ATTNCTTNC 1282

RESULT 9

AAS06711

ID AAS06711 standard; cDNA; 1032 BP.

XX

AC AAS06711;

XX

DT 12-SEP-2001 (first entry)

XX

DE Polynucleotide sequence encoding human protein kinase #11.

XX

KW Human; protein kinase; PTK; STK; cancer; cardiovascular disease;

KW metabolic disorder; immune related disease; neurological disorder;

KW neurodegenerative disorder; inflammatory disorder; infectious disease;

KW reproductive disorder; gene therapy; ss.

XX

OS Homo sapiens.

XX

PN WO200138503-A2.

XX

PD 31-MAY-2001.

XX

PF 22-NOV-2000; 2000WO-US032085.

XX

PR 24-NOV-1999; 99US-0167482P.

XX

PA (SUGE-) SUGEN INC.

XX

PI Plowman GD, Whyte D, Manning G, Sudarsanam S, Martinez R;

PI Flanagan P, Clary D;

XX

DR WPI; 2001-343950/36.

DR P-PSDB; AAU03511.

XX

PT Nucleic acids encoding human kinase polypeptides, useful for preventing

PT diagnosing and/or treating e.g. cancer, immune, cardiovascular and

PT neuronal-associated diseases, and microbial infections.

XX

PS Example 1; Fig 1; 433pp; English.

XX

CC AAS06701-AAS06757 encode for novel human protein kinases #1-57. The novel

CC protein kinases have been identified as members of the tyrosine or

CC serine/threonine kinase (PTK and STK) families. The polynucleotides

CC encoding protein kinases and the polypeptides may be used in the

CC prevention, diagnosis and treatment of diseases associated with

CC inappropriate kinase expression. For example, they may be used to treat

CC cancers (especially cancers of haematopoietic origin), cardiovascular

CC disease (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),

CC immune related diseases (e.g. rheumatoid arthritis), neurological

CC	disorders (e.g. schizophrenia), neurodegenerative disorders (e.g. Parkinson's disease), inflammatory disorders (e.g. asthma), infectious disease (e.g. HIV) and reproductive disorders (e.g. infertility).
CC	Additionally, polynucleotides encoding protein kinases may be used for gene therapy and as DNA probes in diagnostic assays. The protein kinase polypeptides may be used as antigens in the production of antibodies against the protein kinases and in assays to identify modulators of protein kinase expression and activity
XX	
SQ	Sequence 1032 BP; 206 A; 326 C; 307 G; 193 T; 0 U; 0 Other;
Query Match 53.8%; Score 836.8; DB 4; Length 1032;	
Best Local Similarity 88.2%; Pred. No. 2.6e-210;	
Matches 910; Conservative 0; Mismatches 122; Indels 0; Gaps 0;	
QY	105 ATGCTGCTGCTCAAGAAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAAG 164
Db	1 ATGCTGCTGCTGAAGAAACACACGGAGGACATCAGCAGCGTCTACGAGATCCGCGAGAGG 60
QY	165 CTGGGCTCGGGTGCTTCTCTGAGGTGATGTGGGCCCAGGAAAGGGGCTGTGCTCATCTT 224
Db	61 CTCGGCTCGGGTGCTTCTCGAGGTGTTGTGGCCCCAGGAGCGGGCTCCGCACACCTC 120
QY	225 GTGGCCCTCAAGTGCATTCCCAAGAAAGCACTTCGGGGCAAGGAGGCCCTGGTGGAGAT 284
Db	121 GTGGCCCTCAAGTGCATCCCCAAGAGGCCCTCCGGGGCAAGGAGGCCCTGGTGGAGAAC 180
QY	285 GAGATCGCGGTACTTCGCAGAAATCAGCCATCCCCAACATTGTGGCTCTGGAGGACGTCCAT 344
Db	181 GAGATCGCAGTGTCTCGTAGGATCAGTACCCCAACATCGTCGCTCTGGAGGATGTCCAC 240
QY	345 GAGAGTCCTTCTCATCTCTACTTGGCCATGAGCTGGTAACAGGTGTGAACCTGTTTGAC 404
Db	241 GAGAGCCCTTCCACCTCTACCTGGCCATGGAACCTGGTGACGGGTGGCGAGCTGTTTGAC 300
QY	405 CGCATATGGAGGGGGCTCCTACACAGAGAGGACGCCAGCCACCTTGTAGGGCAGGTC 464
Db	301 CGCATATGGAGCGGGCTCCTACACAGAGAGGATGCCAGCCATCTGTGGTTCAGGTC 360
QY	465 CTTGGCGCTGTCTCCTACCTTTCATAGCCTGGGCATCGTGCAACGGGACCTCAAGCCCTGAA 524
Db	361 CTTGGCGCGTCTCCTACCTGCAACGCTGGGATCGTGCAACGGGACCTCAAGCCCGAA 420
QY	525 AACCTCCTCTATGCCACACCTTTTGAGGACTCAAGATCATGGTCTCTGACTTTGGCCTG 584
Db	421 AACCTCCTGTATGCCACGCCCTTTGAGGACTCGAAGATCATGGTCTCTGACTTTGGACTC 480
QY	585 TCCAAAATACAAGCTGGCAACATCTAGGCACAGCCTGTGGGACCCAGATATGTGGCC 644
Db	481 TCCAAAATCCAGGCTGGGAACATGCTAGGCACCGCTGTGGGACCCCTGGATATGTGGCC 540
QY	645 CCAGAGCTCCTGGAGAGAAACCCCTACGGGAAGGCCGTAGATGTGTGGCCCTGGGTGTC 704
Db	541 CCAGAGCTCTTGGAGAGAAACCCCTACGGGAAGGCCGTAGATGTGTGGCCCTGGGCGTC 600
QY	705 ATCTCCTACATCCTGCTGTGTGGTACCCCCCTTCTATGATGAGAGCGGATCCTGAACTC 764
Db	601 ATCTCCTACATCCTGCTGTGTGGTACCCCCCTTCTACGACGAGCGACCCCTGAGCTC 660
QY	765 TTCAGCCAGATTCTGAGGGCCAGCTATGAGTTTGACTCCCCCTTTTGGGATGACATCTCA 824
Db	661 TTCAGCCAGATCCTGAGGGCCAGCTATGAGTTTGACTCTCCTTTCTGGGGTGACATCTCA 720
QY	825 GAATCAGCCAAAGACTTCATTGCGCCACCTTCTGGAACGTGATCCCCAGAGAGGTTTACC 884
Db	721 GAATCAGCCAAAGACTTCATCCGGCACCTTCTGGAGCGAGACCCCCAGAGAGGTTTACC 780
QY	885 TGCCAGCAGGCCCTTACAGCATCTTTGGATCTCTGGGGATGCAGCCTTCGATAGGGACATC 944
Db	781 TGCCAACAGGCCCTTGCGGCACCTTTGGGTCTCTGGGGACACAGCCTTCGACAGGGACATC 840
QY	945 CTGGGTTCTGTGAGTGAGCAGATCCAGAAGAAATTTTGCCAGGACCCACTGGAAGCGTGCA 1004

Db	841 TTAGGCTTGTCAGTGAGCAGATCCGGAAGAACTTTGCTCGGACACACTGGAAGCGAGCC 900
QY	1005 TTCAATGCCACATCATTTCTTACGTACATCCGTAAGCTGGGACAAAGCCAGAGGGTGAG 1064
Db	901 TTCAATGCCACCTCGTTCTCTCGGCCACATCCGGAAGCTGGGGCAGATCCAGAGGGCGAG 960
QY	1065 GAGGCTCCAGGCAGTGTATGACCCGTCATAGCCACCCAGGCCCTTGGGACTAGCCAGTCC 1124
Db	961 GGGGCTCTTGAGCAGGGCATGGCCCGCACAGCCACTCAGGCCCTCCGTGTGGCCAGCCC 1020
QY	1125 CCCAAGTGGTGA 1136
Db	1021 CCCAAGTGGTGA 1032
RESULT 10	
ABZ11323	
ID	ABZ11323 standard; cDNA; 1216 BP.
XX	
AC	ABZ11323;
XX	
DT	20-JAN-2003 (first entry)
XX	
DE	Human polynucleotide SEQ ID NO 205.
XX	
KW	Human; genome mapping; gene therapy; food supplement; virus; fungus; cell-proliferative disorder; neurodegenerative disease; bacterial;
KW	Parkinson's disease; Alzheimer's disease; autoimmune disease;
KW	multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
KW	arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;
KW	antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
KW	haemostatic; vulnery; fungicide; antibacterial; virucide; protozoacide;
KW	antiarthritic; gene; ss.
XX	
OS	Homo sapiens.
XX	
PN	WO200270539-A2.
XX	
PD	12-SEP-2002.
XX	
PF	05-MAR-2002; 2002WO-US005095.
XX	
PR	05-MAR-2001; 2001US-00799451.
XX	
PA	(HYSE-) HYSEQ INC.
XX	
PI	Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
PI	Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
PI	Wehrman T, Wang J, Wang D, Drmanac RT;
XX	
DR	WPI; 2002-759812/82.
DR	P-PSDB; ABP69106.
XX	
PT	New polynucleotides comprising sequences assembled from expressed
PT	sequence tags (ESTs), useful for treating cell-proliferative,
PT	neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
PT	or coagulation disorders.
XX	
PS	Claim 1; SEQ ID NO 205; 1012pp + Sequence Listing; English.
XX	
CC	The invention relates to an isolated polynucleotide (I) comprising a
CC	nucleotide sequence selected from any of 948 sequences (ABZ11119-
CC	ABZ12066) or their mature protein coding portion, active domain coding
CC	protein or complementary sequences. The polynucleotides are useful for
CC	identifying expressed genes or for physical mapping of human genome. The
CC	encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight
CC	markers, as a food supplement, for generating antibodies, in medical
CC	imaging, screening and diagnostic assays and for treating cell-
CC	proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
CC	or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
CC	diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
CC	platelet or coagulation disorders, wound, burns, incision, ulcers, liver
CC	or lung fibrosis, infections (bacterial, viral, fungal, parasitic),

















Qy	1053	CCAGAGG	FTGAGGAGG	CCCTCCAGG	CAGTGTATG	ACCCGTCATAG	CCACCCAGG	CCCTTTGGG	1112
Db	1356	CCAGAGG	CGAGGGG	CGCTCTGAG	CAGGCGATG	GGCCCGCACAG	CCCACTCAGG	CCCTCCGT	1415
Qy	1113	ACTAGCC	AGTCCCC	CAAGTGGT	GAAACCA	CAGGTAGATG	CCCAAGGA	AGGCCAAGTGG	ACTG 1172
Db	1416	GCTGGCC	AGCCCCCA	AGTGGTGT	GATGCCCA	GGCAGATGCC	----GAGG	CCAAAGTGG	ACTG 1471
Qy	1173	ACTCCCG	GTTCCTT	CTCCTCC	AGCCCTT	TTGGTCTCT	1210		
Db	1472	ACCCCA	GATTTCCT	TCCCTT	GGATGCTT	TCGGTCCCT	1509		
RESULT 15									
ADI40898									
ID	ADI40898	standard;	cdna;	1120	BP.				
XX									
AC	ADI40898;								
DT	22-APR-2004	(first entry)							
XX									
DE	Human kinase and phosphatase KPP-11	encoding	cdna	SEQ ID NO:64.					
XX									
KW	human; kinase and phosphatase; KPP; enzyme; cardiovascular;								
KW	antiarteriosclerotic; hypotensive; vasotropic; antiinflammatory;								
KW	antiangular; anti-Hiv; antiallergic; antiasthmatic; immunosuppressive;								
KW	antihypoid; dermatological; antidiabetic; nephrotropic; antigout;								
KW	gastrointestinal; neuroprotective; osteopathic; antiarthritic; uropathic;								
KW	ophthalmological; antirheumatic; antiparkinsonian; nootropic;								
KW	anticonvulsant; hepatotropic; CNS; antipsoriatic; haemostatic;								
KW	cytostatic; antilipaemic; antiparasitic; antihelminthic; antibacterial;								
KW	virucide; protozoacide; fungicide; gene therapy; kinase modulator;								
KW	phosphatase modulator; cardiovascular disease; immune system disorder;								
KW	neurological disorder; growth and development disorder;								
KW	cell proliferative disorder; infection; gene; ss.								
XX									
OS	Homo sapiens.								
XX									
FH	Key	Location/Qualifiers							
FT	CDS	201..569							
FT		/*tag= a							
FT		/product= "kinase and phosphatase KPP-11"							
XX									
PN	WO2004009778-A2.								
XX									
PD	29-JAN-2004.								
XX									
PF	18-JUL-2003; 2003WO-US022650.								
XX									
PR	19-JUL-2002; 2002US-0397354P.								
PR	02-AUG-2002; 2002US-0400509P.								
PR	02-AUG-2002; 2002US-0400783P.								
PR	15-AUG-2002; 2002US-0404027P.								
XX									
PA	(INCY-) INCYTE CORP.								
XX									
PI	Hafalia AJA, Emerling BM, Kable AE, Richardson TW, Becha SD;								
PI	Baughn MR, Tang YT, Lal PG, Lee SY, Griffin JA, Khare R;								
PI	Elliott VS, Jin P, Hawkins PR, Swarnakar A, Chawla NK, Tran UK;								
PI	Gururajan R, Ding L, Marquis JP, Thornton MB, Forsythe IJ, Lee EA;								
PI	Gietzen KJ, Ramkumar J;								
XX									
DR	WPI; 2004-132950/13.								
DR	P-PSDB; ADI40845.								
XX									
PT	New human kinases and phosphatases, useful for diagnosing, treating or								
PT	preventing atherosclerosis, hypertension, AIDS, allergy, multiple								
PT	sclerosis, osteoarthritis, Alzheimer's disease, Crohn's disease, cancer								
PT	or hepatitis.								
XX									
PS	Claim 5; SEQ ID NO 64; 330pp; English.								
XX									

CC	The present sequence encodes a human kinase and phosphatase (KPP)								
CC	protein. KPP sequences have cardiovascular, antiarteriosclerotic,								
CC	hypotensive, vasotropic, antiinflammatory, antiangular, anti-HIV,								
CC	antiallergic, antiasthmatic, immunosuppressive, antithyroid,								
CC	dermatological, antidiabetic, nephrotropic, antigout, gastrointestinal,								
CC	neuroprotective, osteopathic, antiarthritic, uropathic, ophthalmological,								
CC	antirheumatic, antiparkinsonian, nootropic, anticonvulsant, hepatotropic,								
CC	CNS, antipsoriatic, haemostatic, cytostatic, antilipaemic, antiparasitic,								
CC	antihelminthic, antibacterial, virucide, protozoacide and fungicide								
CC	activities, and can be used in gene therapy, as kinase modulators and								
CC	phosphatase modulators. KPP proteins, polynucleotides, agonists and								
CC	antagonists can be used for diagnosing, treating or preventing disorders								
CC	associated with aberrant expression of KPP, such as cardiovascular								
CC	diseases (e.g. atherosclerosis, hypertension, vasculitis, angina pectoris								
CC	or congestive heart failure), immune system disorders (e.g. AIDS,								
CC	allergies, asthma, autoimmune thyroiditis, contact dermatitis, Crohn's								
CC	disease, diabetes mellitus, glomerulonephritis, Goodpasture's syndrome,								
CC	gout, irritable bowel syndrome, multiple sclerosis, osteoarthritis,								
CC	osteoporosis, pancreatitis, Reiter's syndrome, rheumatoid arthritis,								
CC	Sjogren's syndrome or uveitis), neurological disorders (e.g. Alzheimer's								
CC	disease, Parkinson's disease, Huntington's disease, dementia or								
CC	epilepsy), disorders affecting growth and development (e.g. cirrhosis,								
CC	hepatitis, mixed connective tissue disease, psoriasis or primary								
CC	thrombocytopenia), cell proliferative disorders (e.g.								
CC	hypercholesterolaemia, hyperlipidaemia or cancer), or viral, bacterial,								
CC	fungal, parasitic, protozoan or helminthic infections. The KPP and								
CC	polynucleotides are also useful in assessing the effects of exogenous								
CC	compounds on the expression of nucleic acids and kinases and								
CC	phosphatases, or for facilitating the drug discovery process, including								
CC	determination of efficacy, dosage, toxicity and pharmacology. The								
CC	polynucleotides encoding Kpp are useful for creating transgenic animals								
CC	to model human disease.								
XX									
SQ	Sequence 1120 BP; 248 A; 342 C; 328 G; 202 T; 0 U; 0 Other;								
	Query Match 37.9%; Score 588.8; DB 12; Length 1120;								
	Best Local Similarity 76.2%; Pred. No. 8.1e-145;								
	Matches 805; Conservative 0; Mismatches 112; Indels 139; Gaps 1;								
Qy	101	AGACATG	TGCTGCT	CAAGAA	CAGACG	GAGGAC	ATCAG	CAGTGT	CTATGAGATCCGGGA 160
Db	197	AAACATG	TGCTGCT	GAAAGAA	CACACG	GAGGAC	ATCAG	CAGCGT	CTACGAGATCCGCGA 256
Qy	161	GAAGCTG	GGCTCG	GGTGCT	TCTCTG	AGTGAT	GTGCG	CCAGAA	AGGGGCTCTGTCTCA 220
Db	257	GAGGCTC	GGCTCG	GGTGCT	TCTCGG	AGTGCT	GTGCG	CCAGAG	CGGGGCTCCGCACA 316
Qy	221	TCTTGTG	GGCCCT	CAAGTG	CATTCC	CAAGAA	GCAC	TTCGG	GGCAAGGAGGCCCTGGTGA 280
Db	317	CCTCGTG	GGCCCT	CAAGTG	CATCCC	CAAGAA	GCAC	TTCGG	GGCAAGGAGGCCCTGGTGA 376
Qy	281	GAATGAG	ATCGCG	GTACTT	CGCAGA	ATCAG	CCATCC	CAACAT	TGTGGCTCTGGAGGACGT 340
Db	377	GAACGAG	ATCGCAG	TGCTCC	GTAGGAT	CAGTCA	CCCCCA	CATCGT	CGCTCTGGAGGATGT 436
Qy	341	CCATGAG	AGTCCCT	TCTCTCA	TCTACT	TGCGCA	TGGAG	CTGGTA	ACAGGTGGTGAAGTGT 400
Db	437	CCACGAG	AGCCCT	TCCACCT	CTACCT	TGGCCAT	GGA	AACT	----- 475
Qy	401	TGACCGC	ATCATG	GAGCGG	GCTCCT	CACAC	AGAGAG	GACG	CCAGCCACCTTGTAGGGCA 460
Db	476	-----							----- 475
Qy	461	GGTCCTT	GGCGTG	TCTCTCT	TACCTT	CATAGC	CTGGG	CATCGT	GCACCGGGACCTCAAGCC 520
Db	476	-----							-----CC 477
Qy	521	TGAAAAC	CTCCTCT	ATGCCC	ACACCT	TTTGAG	GA	CTCCA	AGATCATGGTCTCTGACTTTGG 580
Db	478	CGAAAAC	CTCCTCT	GTATGC	CCACGC	CTTTG	AGGACT	CGAAG	ATCATGGTCTCTGACTTTGG 537
Qy	581	CCTGTCC	AAAAAT	ACAAG	CTGGCA	ACATG	CTAGG	CACAG	CCCTGTGGGACCCCGGATATGT 640



Db	538	ACTCTCCAAAATCCAGGCTGGGAACATGCTAGGACCGCCTGTGGGACCCCTGGATATGT	597
QY	641	GGCCCCCAGAGCTCCTGGAGCAGAAAAACCTACGGGAAGGCCGCTAGATGTGTGGGCCCTTGGG	700
Db	598	GGCCCCCAGAGCTCCTGGAGCAGAAAAACCTACGGGAAGGCCGCTAGATGTGTGGGCCCTTGGG	657
QY	701	TGTCATCTCCTACATCCTGCTGTGTGGGTACCCCCCTTCTATGATGAGAGCGATCCTGA	760
Db	658	CGTCATCTCCTACATCCTGCTGTGTGGGTACCCCCCTTCTACGACGAGAGCGACCCCTGA	717
QY	761	ACTTTTCAGCCAGATTCTGAGGGCCAGCTATGAGTTTGACTCCCCCTTTTGGGATGACAT	820
Db	718	GCTCTTCAGCCAGATCCTGAGGGCCAGCTATGAGTTTGACTCTCCTTTCTGGGATGACAT	777
QY	821	CTCAGAATCAGCCAAAGACTTCATTGCGCCACCTTCTGGAAAGTGATCCCCCAGAAAGAGTT	880
Db	778	CTCAGAATCAGCCAAAGACTTCATTGCGCCACCTTCTGGAGCGAGACCCCCAGAAAGAGTT	837
QY	881	CACCTGCCAGCAGGCCCTACAGCATCTTTGGATCTCTGGGGATGCAGCCTTCGATAGGGA	940
Db	838	CACCTGCCAACAGGCCCTTGGGCACCTTTGGATCTCTGGGGACACAGCCTTCGACAGGGA	897
QY	941	CATCCTGGGTTCTGTCAAGTGCAGATCCAGAAAGATTTGCCAGGACCCACTGGAAGCG	1000
Db	898	CATCTTAGGCTCTGTCAAGTGCAGATCCGGAAGAACTTTGCTCGGACACACTGGAAGCG	957
QY	1001	TGCATTCAATGCCACATCATTCCTACGTACATCCGTAAGCTGGGACAAAGCCAGAGGG	1060
Db	958	AGCCTTCAATGCCACCTCGTTCTGCGCCACATCCGGAAGCTGGGCAGATCCAGAGGG	1017
QY	1061	TGAGGAGGCCCTCCAGGCAGTGTATGACCCGTATAGCCACCCAGGCCCTTGGGACTAGCCA	1120
Db	1018	CGAGGGGGCCTCTGAGCAGGGCATGGCCCGCCACAGCCACTCAGGCCCTCCGTGCTGGCCA	1077
QY	1121	GTCCCCCAAGTGGTGAACCAAGGTAGATGCCAAGG	1156
Db	1078	GCCCCCAAGTGGTGTATGCCCAGGCAGATGCCGAGG	1113

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GenCore version 5.1.6  
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QM nucleic - nucleic search, using sw model

Run on: June 5, 2005, 23:59:55 ; Search time 409 Seconds  
(without alignments)  
6217.051 Million cell updates/sec

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Perfect score: 1554  
Sequence: 1 gttgcggagtcctccactc.....caaaaaaaaaaaaaaaaaa 1554

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/ina/PCtUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		DB ID	Length	Description
	Score	Match			
1	1261.2	81.2	1458	4	US-09-230-896C-5 Sequence 5, Appli
2	859	55.3	1584	4	US-09-799-451-205 Sequence 205, Appl
3	844.4	54.3	1282	2	US-08-878-989-12 Sequence 12, Appl
4	844.4	54.3	1282	3	US-09-272-796-12 Sequence 12, Appl
5	844.4	54.3	1282	4	US-09-016-434-953 Sequence 953, Appl
6	500.8	32.2	1442	4	US-09-949-016-1590 Sequence 1590, Ap
7	500.8	32.2	1442	4	US-09-949-016-1591 Sequence 1591, Ap
8	500.8	32.2	1480	4	US-09-016-434-1454 Sequence 1454, Ap
9	436.2	28.1	1074	4	US-09-733-388-3 Sequence 3, Appli
10	436.2	28.1	1074	4	US-10-446-175-3 Sequence 3, Appli
11	436.2	28.1	1158	4	US-09-733-388-1 Sequence 1, Appli
12	436.2	28.1	1158	4	US-10-446-175-1 Sequence 1, Appli
13	436.2	28.1	1671	4	US-09-733-388-5 Sequence 5, Appli
14	436.2	28.1	1671	4	US-10-446-175-5 Sequence 5, Appli
15	436.2	28.1	1733	4	US-09-620-312D-526 Sequence 526, App
16	428.4	27.6	2447	4	US-09-960-643-1 Sequence 1, Appli
17	428.2	27.6	1694	4	US-09-579-664B-3 Sequence 3, Appli
18	428.2	27.6	1694	4	US-10-355-975A-3 Sequence 3, Appli
19	399	25.7	2165	4	US-09-620-312D-809 Sequence 809, App
20	251.8	16.2	1503	4	US-09-797-039-3 Sequence 3, Appli
21	251.8	16.2	2297	4	US-09-797-039-1 Sequence 1, Appli
22	251.8	16.2	2747	4	US-09-620-312D-19 Sequence 19, Appl
23	251.8	16.2	2840	4	US-09-620-312D-20 Sequence 20, Appl
24	251.8	16.2	3124	3	US-09-734-030-1 Sequence 1, Appli
25	251.8	16.2	3124	4	US-10-153-921-1 Sequence 1, Appli
26	251.8	16.2	3124	4	US-10-669-689-1 Sequence 1, Appli
27	218.2	14.0	781	4	US-09-016-434-851 Sequence 851, App

28	217.8	14.0	3471	2	US-08-715-568A-2	Sequence 2, Appli
29	196.8	12.7	2454	4	US-09-992-481-3	Sequence 3, Appli
30	196.8	12.7	2454	4	US-10-434-034-3	Sequence 3, Appli
31	196.8	12.7	2824	4	US-09-992-481-5	Sequence 5, Appli
32	196.8	12.7	2824	4	US-10-434-034-5	Sequence 5, Appli
33	188	12.1	2298	4	US-09-975-326-3	Sequence 3, Appli
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35	188	12.1	2301	4	US-09-975-326-1	Sequence 1, Appli
36	188	12.1	2301	4	US-10-217-357-1	Sequence 1, Appli
37	181.8	11.7	5703	4	US-09-949-016-673	Sequence 673, App
38	181.8	11.7	5703	4	US-09-949-016-4012	Sequence 4012, Ap
39	181.8	11.7	5708	4	US-09-566-921-21	Sequence 21, Appl
40	177	11.4	2218	4	US-09-820-790B-1	Sequence 1, Appli
41	175.4	11.3	2061	3	US-09-800-960-1	Sequence 1, Appli
42	175.4	11.3	2061	4	US-10-096-960-1	Sequence 1, Appli
43	168.6	10.8	2157	4	US-09-949-016-1966	Sequence 1966, Ap
44	167.6	10.8	1429	2	US-09-159-385-4	Sequence 4, Appli
45	167.6	10.8	1429	3	US-09-186-277-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1  
US-09-230-896C-5  
; Sequence 5, Application US/09230896C  
; Patent No. 6635479  
; GENERAL INFORMATION:  
; APPLICANT: The Scripps Research Institute  
; APPLICANT: Sutcliffe, et al.  
; TITLE OF INVENTION: Hypothalamus-Specific Polypeptides  
; FILE REFERENCE: TSRI-548.1  
; CURRENT APPLICATION NUMBER: US/09/230,896C  
; CURRENT FILING DATE: 1999-02-02  
; PRIOR APPLICATION NUMBER: 60/023,220  
; PRIOR FILING DATE: 1996-08-02  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 1458  
; TYPE: DNA  
; ORGANISM: ratus ratus  
US-09-230-896C-5

Query Match		81.2%;	Score 1261.2;	DB 4;	Length 1458;
Best Local Similarity		93.6%;	Pred. No. 0;		
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				Indels	29;
				Gaps	2;
Qy	99	GCAGACATGCTGCTGCTCAAGAAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGG	158		
Db	44	GCAGACATGCTGCTGCTCAAGAAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGG	103		
Qy	159	GAGAAGCTGGGCTCGGGTGCCTTCTCTGAGGTGATGCTGGCCCCAGGAAAGGGCTCTGCT	218		
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Qy	219	CATCTTGTGGCCCTCAAGTGCATTCCCAAGAAAGCACTTCGGGGCAAGGAGGCCCTGGTG	278		
Db	164	CATCTTGTGGCCCTCAAGTGCATTCCCAAGAAAGCACTTCGGGGCAAGGAGGCCCTGGTG	223		
Qy	279	GAGAATGAGATCGCGGTACTTCGCAGAATCAGCCATCCCAACATTGTGGCTCTGGAGGAC	338		
Db	224	GAGAATGAGATCGCAGTACTCCGCAGGATTAGCACCCCAACATTGTGGCTCTGGAGGAC	283		
Qy	339	GTCCATGAGAGTCCTTCTCATCTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAAGTG	398		
Db	284	GTCCACGAGAGGCCCTTCCCATTCTACTTTGGCCATGGAGCTGGTAACAGGTGGTGAAGTG	343		
Qy	399	TTTGACCGCATCATGGAGCGGGGCTCCTACACAGAGAGGACGCCACCTTGTAGGG	458		
Db	344	TTTGACCGCAATCATGGAGCGGGGCTCCTACACAGAGAGGATCGGAGCCACCTTGTAGGG	403		
Qy	459	CAGGTCCTTGGCGGTGTCTCTACCTTTCATAGCTGGGCATCGTGCACCCGGGACCTCAAG	518		



Db 404 CAGGTCCCTTGGTGTCTCTCTACCTTATAGCCTGGGCATCGTGACCGGACCTCAAG 463

QY 519 CCTGAAACCTCTCTATGCCACACCTTTTGGAGACTCCAAGATCATGGTCTCTGACTTT 578

Db 464 CCTGAAACCTCTCTATGCCACACCTTTTGGAGACTCCAAGATCATGGTCTCTGACTTT 523

QY 579 GGCCTGTCCAAAATACAAAGCTGGCAACATGCTAGGCACAGCCTGTGGACCCCCAGGATAT 638

Db 524 GGCCTGTCCAAAATTCAAAGCTGGCAACATGCTAGGCACAGCCTGTGGACCCCCAGGATAT 583

QY 639 GTGGCCCCAGAGCTCCTGGAGCAGAAACCCCTACGGGAAGGCCGTAGATGTGTGGGCCCTG 698

Db 584 GTGGCCCCAGAGCTCCTGGAGCAGAAACCCCTACGGGAAGGCCGTAGATGTGTGGGCCCTG 643

QY 699 GGTGTATCTCTACATCCTGTCTGTGTGGGTACCCCCCTTCTATATGATGAGCGATCCT 758

Db 644 GGTGTATCTCTACATCCTGTCTGTGTGGGTACCCCCCTTCTATATGATGAGCGATCCT 703

QY 759 GAACCTCTTACAGCCAGATTCTGAGGGCCAGCTATGAGTTTGACTCCCCCTTTGGGATGAC 818

Db 704 GAACCTCTTACAGCCAGATTCTGAGGGCCAGCTATGAGTTTGACTCTCCCTTTGGGATGAC 763

QY 819 ATCTCAGAAATCAGCCAAAAGACTTCATTGCGACACCTTCTGGAACGTGATCCCCAGAGAGG 878

Db 764 ATCTCAGAAATCAGCCAAAAGACTTCATTGCGACACCTTCTGGAACGTGATCCCCAGAGAGG 823

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Db 944 CGTGCAATTCATGSCACATCATTCCTACGTACATCCGTAAGCTGGGACAGAGCCCAGAG 1003

QY 1059 GGTGAGGAGGCCTCCAGGCAGTGTATGACCCGTATAGCCCATAGCCACCCAGGCCTTGGACTAGC 1118

Db 1004 GGTGAGGAGGCCTCCAGGCAGGTATGACCCGTACAGCCACCCAGGCCTTGGACTAGC 1063

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Db 1064 CAGTCTCCCAAGTGGTGAATAACAGGTGGATGCCAAGGAAGGCCAAGTGGACTGACTCCT 1123

QY 1179 GGTTTTCTTTCTCCAGGCCCTTTTGGTCTCTTTCTCTGGATCCTTGTCTCCAGACTGGC 1238

Db 1124 AGCTTTTCTTTCTCCAGGCCCTTTTGATCTCTCTCCCTGATCCTTTGTCCCGGACTGGC 1183

QY 1239 CTCTGTCTGGAAGTCTGAGAC--TGGGTGTGATGCATGGCACTAGGGTACGGGGCTTCCC 1296

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QY 1297 CAGTATGTCCCCCAGCCTCTATTCTTACCTATGGTGGAGGCTCCCTTTCCCATGTGCTG 1356

Db 1244 AAGTATGTCCCC-----AGCCTCTGTCTTTGTGTGCTG 1276

QY 1357 CCACCCCTCTATGGAAGTCTGAGAGGTGTTCAAAGTGGACTTGGGAGCCATCCTTCCCTGC 1416

Db 1277 CCACCCCTCTATGGAAGTCTGAGAGGTATTCAAATAATGGATTGGGGGCCATCCTTCCCTGC 1336

QY 1417 ACCTTGCAAGAACACATGCATTGTGTGGCTGTCTGTGCTTTGCTGACTGTGGGTGGTCC 1476

Db 1337 ACCTTGCAAGCACATATGCATTGCGTGGCTGTCTGTGCTTTGCTGACTGTGGGTGGTCC 1396

QY 1477 TGCTTGTGTGTGGCCCTTTTAGTTCCTCCTTTTCTAACCAATAAAGACAAACAGAACCA 1536

Db 1397 TGCTTGTGTGTAGCCCTTTTAGTTCCTCCTCTTTCCAACCAATAAAGACAAACAGAACAA 1456

US-09-799-451-205

; Sequence 205, Application US/09799451

; Patent No. 6783969

; GENERAL INFORMATION:

; APPLICANT: Tang, Y. Tom

; APPLICANT: Zhou, Ping

; APPLICANT: Goodrich, Ryle

; APPLICANT: Asundi, Vinod

; APPLICANT: Ren, Feiyan

; APPLICANT: Zhang, Jie

; APPLICANT: Xue, Aidong J.

; APPLICANT: Zhao, Qing A.

; APPLICANT: Wang, Jian-Rui

; APPLICANT: Ma, Yunging

; APPLICANT: Yamazaki, Victoria

; APPLICANT: Chen, Rui-hong

; APPLICANT: Wang, Zhiwei

; APPLICANT: Wang, Dunrui

; APPLICANT: Yang, Yonghong

; APPLICANT: Wehrman, Tom

; APPLICANT: Ghosh, Reena

; APPLICANT: Drmanac, Radoje T.

; TITLE OF INVENTION: No. 6783969el Nucleic Acids and

; TITLE OF INVENTION: Polypeptides

; FILE REFERENCE: 803

; CURRENT APPLICATION NUMBER: US/09/799,451

; NUMBER OF SEQ ID NOS: 948

; SOFTWARE: pt\_FL\_genes Version 2.0

; SEQ ID NO 205

; LENGTH: 1584

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (51)..(1166)

US-09-799-451-205

Query Match 55.3%; Score 859; DB 4; Length 1584;

Best Local Similarity 78.7%; Pred.No. 1e-252;

Matches 1098; Conservative 0; Mismatches 270; Indels 27; Gaps 5;

QY 168 GGCTCGGGTGCCTTCTCTGAGGTGATGCTGGCCCCAGGAAAGGGGCTCTGCTCATCTTGTG 227

Db 201 GGCAGGGTGCCTTCTCCAGGTGGTGTGGTGGCCCCAGGAGCGGGCTCCGCACACCTCGTG 260

QY 228 GCCCTCAAGTGCATTCCTCAAGAAAGCACTTCGGGGCAAGAGGCCCTGGTGAGAAATGAG 287

Db 261 GCCCTCAAGTGCATTCCTCAAGAAAGGCCCTCCGGGGCAAGAGGCCCTGGTGAGAAACGAG 320

QY 288 ATCGCGGTACTTCGAGAAATCAGCCATCAGCCATCCCAACATTTGGCTCTCGGAGGAGTCCATGAG 347

Db 321 ATCGCAGTGTCCGTAGGATCAGTCACCCCAACATCGTCGCTCTGGAGGATGTCCACGAG 380

QY 348 AGTCCTTCTCATCTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAACCTGTTGACCGC 407

Db 381 AGCCCTTCCACCTCTACCTGGCCATGGAACCTGGTGACGGTGGCGAGCTGTTGACCGC 440

QY 408 ATCATGGAGCGGGCTCCTACACAGAGAAGGACGCCAGCCACCTTGTAGGGCAGGTCCCTT 467

Db 441 ATCATGGAGCGGGCTCCTACACAGAGAAGGATGCCAGCCATCTGGTGGGTGAGTCCCTT 500

QY 468 GGCCTGTCTCCTACCTTCTATAGCCTGGGCATCGTGCAACCGGACCTCAAGCCTGAAAC 527

Db 501 GGCCTGTCTCCTACCTTGCAAGCCTGGGATCGTGCAACCGGACCTCAAGCCTGAAAC 560

QY 528 CTCTCTATGCCACACCTTTTGAGGACTCCAAAGATCATGGTCTCTGACTTTGGCCTGTCC 587

Db 561 CTCTCTGTATGCCACGCCCTTTTGAGGACTCGAAGATCATGGTCTCTGACTTTGGACTCTCC 620

QY 588 AAAATACAAGCTGGCAACATGCTAGGCACAGCCTGTGGGACCCCGAGGATATGTGGCCCCA 647

Db 621 AAAATCCAGGCTGGGAACATGCTAGGCACCGCCTGTGGGACCCCTGGATATGTGGCCCCA 680



QY 461 GGTCTTGGCGGTGTCTCTACCTTCATAGCCTGGGCATCGTGACCGGGACCTCAAGCC 520  
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Db 557 GGTCTTGGCGCGTCTCTACCTGTCACAGCCTGGGGATCGTGACCGGGACCTCAAGCC 616  
QY 521 TGA AACCTCTCTATGCCACACCTTTTGAGGACTCCAAGATCATGCTCTCTGACTTTGG 580  
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Db 617 CGAA AACCTCTGTATGCCACGCCCTTTGAGGACTCGAAGATCATGCTCTCTGACTTTGG 676  
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Db 677 ACTCTCCAAAATCCAGGCTGGGAACATGCTAGGCACCGCCTGTGGGACCCCTGGATATGT 736  
QY 641 GGCCCCAGAGCTCCTGGAGCAGAAACCCCTACGGGAAGGCCGTAGATGTGTGGGCCCTGGG 700  
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Db 737 GGCCCCAGAGCTCTTGGAGCAGAAACCCCTACGGGAAGGCCGTAGATGTGTGGGCCCTGGG 796  
QY 701 TGTATCTCTACATCTCTGCTGTGTGGGTACCCCCCTTCTATGATGAGAGCGATCCTGA 760  
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Db 797 CGTCATCTCTACATCTCTGCTGTGTGGGTACCCCCCTTCTACGACGAGAGCGACCCTGA 856  
QY 761 ACTCTTCAGCCAGATTTCTGAGGGCCAGCTATGAGTTTGACTCCCCCTTTTGGGATGACAT 820  
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Db 857 GCTCTTCAGCCAGATCCTGAGGGCCAGCTATGAGTTTGACTNTCTTCTTGGGATGACAT 916  
QY 821 CTCAGAATCAGCCAAAGACTTTCATTCGCCCACTTCTGGAACGTGATCCCCCAGAGAGTT 880  
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Db 917 CTCAGAATCAGCAAGACTTTATTTCGGCACTTCTGGAGCGAGACCTTCAGAAGAGTT 976  
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Db 977 CACCTGCCAACAGGCCCTTGCGGGACCTTTGGATCTTTTGGGACACAGGCTTTGGCAGGGA 1036  
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Db 1037 CATCTTAGGTTTGTCTAGTGAGCAGATCCGGAAGAACTTTGCTTGGACACACTGGAAGCG 1096  
QY 1001 TGCATTCAATGCCACATCATTCCTACGTACATCCGTAAAGCTGGGACAAAGCCCCAGAGGG 1060  
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Db 1097 AGCCTTCAATGCCACCTTGTTCCTGCGCCACATCCGGAAGCTGGGCGAGATCCAGAGGG 1156  
QY 1061 TGAGGAGGCCTCCAGGCAGTGTATGACCCGTATAGCCCATAGCCACCCAGGCCTTGGGACTAGCCA 1120  
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Db 1157 CGAGGGGCCTCTGAGCAGGGCATGGSCCGNCACAGCCACTNAGGCCTTCGTCTGGCCA 1216  
QY 1121 GTCCCCCAAGTGTGAAAACCAAGGTAGATGCCAAGGAAGGCCAAGTGGACTGACTCCCCG 1180  
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Db 1217 GCCCCCCAAGTGTGATGCCAGGNAGATGCC----GAGGCCAAGTGGANTGANCCCCAG 1272  
QY 1181 TTTTCTTTTC 1190  
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Db 1273 ATTNCTTNC 1282

RESULT 4  
US-09-272-796-12  
; Sequence 12, Application US/09272796  
; Patent No. 6207148

; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Corley, Neil C.  
; APPLICANT: Guegler, Karl G.  
; APPLICANT: Lal, Preeti  
; APPLICANT: Goli, Surva K.  
; APPLICANT: Shah, Purvi  
; TITLE OF INVENTION: DISEASE ASSOCIATED PROTEIN  
; TITLE OF INVENTION: KINASES  
; NUMBER OF SEQUENCES: 21  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto

; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/272,796  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/878,989  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J J  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0321 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; TELEX:  
; INFORMATION FOR SEO ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1282 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: PROSNOT06  
; CLONE: 827431  
US-09-272-796-12

Query Match 54.3%; Score 844.4; DB 3; Length 1282;  
Best Local Similarity 86.2%; Pred. No. 2.7e-248;  
Matches 940; Conservative 1; Mismatches 145; Indels 4; Gaps 1;  
QY 101 AGACATGCTGCTCAAGAAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGGGA 160  
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Db 197 AAACATGCTGCTGAAGAAACACACGGAGGACATCAGCAGCGTCTACGAGATCCGCGA 256  
QY 161 GAAGCTGGGCTCGGGTGCCCTTCTCTGAGGTGATGCTGGCCCCAGGAAAGGGCTCTGCTCA 220  
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Db 257 GAGGCTCGGCTCGGGTGCCCTTCTCCGAGTGGTGTGGCCCCAGGAGCGGGCTCCGCACA 316  
QY 221 TCTTGTGGCCCTCAAGTGCATTCCTCAAGAAAGCACTTCGGGGCAAGGAGCCCTGGTGGA 280  
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Db 317 CCTCGTGGCCCTCAAGTGCATCCCCAAGAGGCCCTCCGGGGCAAGGAGGCCCTGGTGGA 376  
QY 281 GAATGAGATCGCGGTACTTCGCAGAAATCAGCCCATCCCAACATTTGGTCTCGGAGGACGT 340  
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Db 377 GAACGAGATCGCAGTGTCCGTAGGATCAGTCACCCCAACATCGTCGCTCTGGAGGATGT 436  
QY 341 CCATGAGAGTCCCTTCTCATCTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAACCTGTT 400  
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Db 437 CCACGAGAGCCCTTCCCACCTCTACCTGGCCATGGAACCTGGTGACGGGTGGCGAGCTGTT 496  
QY 401 TGACCGCATCATGGAGCGGGGCTCCTACACAGAGAAGGACGCCAGCCACCTTGTAGGGCA 460  
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Db 497 TGACCGCATCATGGAGCGGGCTCCTACACAGAGAAGGATGCCAGCCATCTGGTGGGTCA 556  
QY 461 GGTCTTGGCGCTGTCTCCTACCTTCTATAGCCTGGGCATCGTGACCCGGACCTCAAGCC 520  
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Db 557 GGTCTTGGCGCGTCTCCTACCTGCACAGCCTGGGGATCGTGACCCGGGACCTCAAGCC 616  
QY 521 TGA AACCTCCTCTATGCCACACCTTTTGAGGACTCCAAGATCATGCTCTCTGACTTTGG 580  
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Db 617 CGAA AACCTCCTGTATGCCACGCCCTTTGAGGACTCGAAGATCATGCTCTCTGACTTTGG 676  
QY 581 CCTGTCCAAAATACAAGCTGGCAACATGCTAGGCACAGCCTGTGGGACCCCAAGGATATGT 640  
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Db 677 ACTCTCCAAAATCCAGGCTGGGAACATGCTAGGCACCGCCTGTGGGACCCCTGGATATGT 736



QY	641	GGCCCCAGAGCTCTGGAGCAGAAACCCCTACGGGAAGGCCGTAGATGTGTGGGCCCTGGG	700
Db	737	GGCCCCAGAGCTCTTGGAGCAGAAACCCCTACGGGAAGGCCGTAGATGTGTGGGCCCTGGG	796
QY	701	TGTCATCTCCTACATCCTGCTGTGTGGGTACCCCCCTTCTATGATGAGAGCGCATCCTGA	760
Db	797	CGTCATCTCCTACATCCTGCTGTGTGGGTACCCCCCTTCTACGACGAGAGCGACCCCTGA	856
QY	761	ACTCTTCAGCCAGATTCTGAGGGCCAGCTATGAGTTTGACTCCCCCTTTTGGGATGACAT	820
Db	857	GCTCTTCAGCCAGATCCTGAGGGCCAGCTATGAGTTTGACTNTCTTCTCTGGGATGACAT	916
QY	821	CTCAGAAATCAGCCAAAGACTTCATTGCGCCACCTTCTGGAAACGTGATCCCACAGAAAGGTT	880
Db	917	CTCAGAAATCAGGCAAAGACTTTATTGCGCACCTTCTGGAGCGAGACCCTTCAGAAGAGGTT	976
QY	881	CACCTGCCAGCAGGCCCTPACAGCATCTTTGGATCTCTGGGGATGCAGCCCTTCGATAGGGA	940
Db	977	CACCTGCCAAACAGGCCCTTGC GGACCTTTGGATCTTTTGGGACACAGGCTTTTGGCAGGGA	1036
QY	941	CATCCTGGGTTCTGTCACTGAGCAGATCCAGAAAGATTTTGCCAGGACCCACTGGAAGCG	1000
Db	1037	CATCTTAGGGTTTGTCACTGAGCAGATCCGGAAGAACTTTGCTTGGACACACTGGAAGCG	1096
QY	1001	TGCATTCAATGCCACATCATTTCTACGTACATCCGTAAGCTGGGACAAAGCCAGAGGG	1060
Db	1097	AGCCTTCAATGCCACCTGTTCTGCGCCACATCCGGAAGCTGGGCGAGATCCAGAGGG	1156
QY	1061	TGAGGAGGCCCTCCAGGCAGTGTATGACCCGTATAGCCACCCAGGCCCTTGGGACTAGCCA	1120
Db	1157	CGAGGGGGCCTCTGAGCAGGGCATGGSCCGNCAAGCCACTNAGGCCCTTCGTGTGGCCA	1216
QY	1121	GTCCCCCAAGTGGTGAAGAACAGGTAGATGCCAAGGAAGGCCAAGTGGACTGACTCCCCG	1180
Db	1217	GCCCCCAAGTGGTGTATGCCCAGGNAGATGCC----GAGGCCAAGTGGANTGANCCCCAG	1272
QY	1181	TTTTTCTTTT	1190
Db	1273	ATTNCTTNC	1282

## RESULTS

US-09-016-434-953  
; Sequence 953, Application US/09016434  
; Patent No. 6500938  
; GENERAL INFORMATION:  
; APPLICANT: Janice Au-Young  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING  
; NUMBER OF SEQUENCES: 1490  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/016,434  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:







QY	539	CACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTGGCCCTGTCCAAAATACAAG-	597
Db	597	CAGCCTGGATGAAGACTCCAAAATCATGATCTCCGACTTTGGCCCTCTCCAAGATGGAGGA	656
QY	598	--CTGGCAACATGTGTAGGCACAGCCTGTGGGACCCAGGATATGTGGCCCGCAGAGCTCCT	655
Db	657	CCCGGCAGTGTGCTCTCCACCGCCTGTGGAACTCCGGGATACGTGGCCCTGGAAGTCTCT	716
QY	656	GGAGCAGAAACCCCTACGGGAAGGCCGTAGATGTGTGGCCCTGGGTGTCATCTCCTACAT	715
Db	717	GGCCAGAAAGCCCTACAGCAAGGCTGTGGATTGCTGGTCCATAGGTGTCTATCGCCTACAT	776
QY	716	CCTGCTGTGTGGGTACCCCCCTTCTATGATGAGAGCGATCCTGAACCTTTCAGCCAGAT	775
Db	777	CTTGCTCTGCGGTACCCCTCCCTTCTATGACGAGAATGATGCCAACTCTTTGAAACAGAT	836
QY	776	TCTGAGGCCAGCTATGAGTTTGACTCCCCCTTTTGGGATGACATCTCAGAATCAGCCAA	835
Db	837	TTTGAAGGCCGAGTACGAGTTTGACTCTCCTTACTGGGACGACATCTCTGACTCTGCCAA	896
QY	836	AGACTTCATTGCGCACCTTCTGGAAAGTGTATCCCAGAAAGAGTTTCACTGTCCAGCAGGC	895
Db	897	AGATTTTCATCCGGCACTTGATGGAGAAGGACCCAGAGAAAAGATTCACTGTGAGCAGGC	956
QY	896	CCTACAGCATCTTTGGATCTCTGGGGATGCAGCCTTCGATAGGGACATCCTGGGTTCTGT	955
Db	957	CTTGCAGCACCCCATGGATTGCAGGAGATACAGCTCTAGATAAGAATATCCACCAGTCGGT	1016
QY	956	CAGTGAGCAGATCCAGAAAGAATTTTGCCAGGACCCACTGGAAGCGTGCATTCAATGCCAC	1015
Db	1017	GAGTGAGCAGATCAAGAAGAACTTTGCCAAGAGCAAGTGAAGCAAGCCTTCAATGCCAC	1076
QY	1016	ATCATTCCTACGTACATCCGTAAGCTG	1043
Db	1077	GGCTGTGGTGGGCACATGAGGAAACTG	1104

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RESULT 9
US-09-733-388-3
; Sequence 3, Application US/09733388
; Patent No. 6602698
; GENERAL INFORMATION:
; APPLICANT: Donoho, Greg
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Abuin, Alejandro
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6602698e1 Human Kinase Proteins and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0103-USA
; CURRENT APPLICATION NUMBER: US/09/733,388
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,428
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1074
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-733-388-3

```

[illegible]

RESULT 10  
US-10-446-175-3  
; Sequence 3, Application US/10446175  
; Patent No. 6806073  
; GENERAL INFORMATION:  
; APPLICANT: Donoho, Greg  
; APPLICANT: Scoville, John  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Abuin, Alejandro  
; APPLICANT: Sands, Arthur T.

; TITLE OF INVENTION: No. 6806073el Human Kinase Proteins and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0103-USA
; CURRENT APPLICATION NUMBER: US/10/446,175
; CURRENT FILING DATE: 2003-05-27
; PRIOR APPLICATION NUMBER: US/09/733,388
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,428
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1074
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-446-175-3

Query Match 28.1%; Score 436.2; DB 4; Length 1074;
Best Local Similarity 67.6%; Pred. No. 4.6e-123;
Matches 628; Conservative 0; Mismatches 298; Indels 3; Gaps 1;

QY 117 AAGAAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAGCTGGGCTCGGGT 176
Db 37 AAAAAAGCAAGCTGAAGACATCAAGAAGATCTTCGAGTTCAAGAGACCCCTCGGACCGGG 96

QY 177 GCCTTCTCTGAGGTGATGCTGGCCCCAGGAAAGGGGCTCTGTCTCATCTTTGTGGCCCTCAAG 236
Db 97 GCCTTTTCCGAAGTGGTTTAGCTGAAGAGAAAGGCAACTGGCAAGCTCTTTGCTGTGAAG 156

QY 237 TGCATTTCCCAAGAAAGCACTTCGGGGCAAGGAGGCCCTGGTGGAGAAATGAGATCGCGGTA 296
Db 157 TGTATCCCTAAGAAAGGCGCTGAAGGGCAAGGAAAGCAGCATAGAGAATGAGATAGCCGTC 216

QY 297 CTTGCGCAGAATCAGCCATCCCAACATTTGTGGCTCTGGAGGACGTCCATGAGAGTCTTCT 356
Db 217 CTGAGAAAGATTAAAGCATGAAATAATTGTTGCCCTGGAAGACATTTATGAAAGCCCAAAT 276

QY 357 CATCTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAACCTGTTTGACCGCATCATGGAG 416
Db 277 CACCTGTACTTGGTCTATGAGCTGGTGTCCGGTGGAGAGCTGTTTGACCGGATAGTGGAG 336

QY 417 CGGGGCTCCTACACAGAGAAGGACGCCAGCCACCTTGTAGGGCAGGTCTTGGCGCTGTC 476
Db 337 AAGGGGTTTATACAGAGAAGGATGCCAGCACTCTGATCCGCCAAAGTCTTTGGACGCCGTG 396

QY 477 TCCTACCTTCATAGCCTGGGATCGTGCACCGGGACCTCAAGCCTGAAAAACCTCTCTAT 536
Db 397 TACTATCTCCACAGAATGGGCATCGTCCACAGAGACCTCAAGCCCGAAAAATCTCTGTAC 456

QY 537 GCCACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTGGCCTGTGCCAAATACAA 596
Db 457 TACAGTCAAGATGAGGAGTCCAAAATAATGATCATGAGTCTTGGATTGTCAAAAATGGAG 516

QY 597 G---CTGGCAACATGCTAGSCACAGCCTGTGGGACCCAGGATATGTGGCCCCCAGAGCTC 653
Db 517 GGCAAGGAGATGTGATGTCCACTGCCCTGTGGAACTCCAGGCTATGTCGCTCCTGAAATC 576

QY 654 CTGGAGCAGAAACCCCTACGGGAAGGCCGTAGATGTGTGGGCCCTGGGTGTCTCTCTAC 713
Db 577 CTCGCCCAGAAACCTTACAGCAAGCCGTTTGA CTGCTGGTCCATCGGAGTGATTCCTTAC 636

QY 714 ATCTGTGTGTGGGTACCCCCCTTCTATGATGAGAGCGATCCTGAACCTTTTCAGCCAG 773
Db 637 ATCTGTCTCTGCGGCTACCCCTCTTTTATGATGAAATGACTCCAAGCTCTTTGAGCAG 696

QY 774 ATTCTGAGGGCCAGCTATGAGTTTGACTCCCCCTTTTGGGATGACATCTCAGAATCAGCC 833
Db 697 ATCCTCAAGGCGGAATATGAGTTTGACTCTCCCTACTGGGATGACATCTCCGACTTGCA 756

QY 834 AAAGACTTCATTTCGCCACCTTCTTGGAACTGATCCCCAGAAAGAGTTTCACCTGCCAGCAG 893
Db 757 AAAGACTTCATTTCGGAACTGATGGGAAGGACCCCGAATAAAGATACACCGTGTGAGCAG 816

QY 894 GCCCTACAGCATCTTTGGATCTCTGGGGATGCAGCCCTTCGATAGGGACATCTCGGGTTCT 953
Db 817 GCAGCTCGGCACCCATGGATCGTGGTGACACAGCCCTCAACAAAAACATCCACGAGTCC 876

QY 954 GTCAGTGAGCAGATCCAGAAGAAATTTGCCAGGACCCACTGGAAAGCGTGCATTCATGACC 1013
Db 877 GTCAGCGCCAGATCCGAAAAAACTTTGCCAAGAGCAAATGGAGACAAGCATTTAATGACC 936

QY 1014 ACATCATTCCTACGTCAACATCCGTAAGCT 1042
Db 937 ACGGCCGTCGTGAGACATATGAGAAAACT 965

RESULT 11
US-09-733-388-1
; Sequence 1, Application US/09733388
; Patent No. 6602698
; GENERAL INFORMATION:
; APPLICANT: Donoho, Greg
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Abuin, Alejandro
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6602698el Human Kinase Proteins and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0103-USA
; CURRENT APPLICATION NUMBER: US/09/733,388
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,428
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1158
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-733-388-1

Query Match 28.1%; Score 436.2; DB 4; Length 1158;
Best Local Similarity 67.6%; Pred. No. 4.8e-123;
Matches 628; Conservative 0; Mismatches 298; Indels 3; Gaps 1;

QY 117 AAGAAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAGCTGGGCTCGGGT 176
Db 37 AAAAAAGCAAGCTGAAGACATCAAGAAGATCTTCGAGTTCAAGAGAGACCCCTCGAACC G 96

QY 177 GCCTTCTCTGAGGTGATGCTGGCCCCAGGAAAGGGGCTCTGCTCATCTTTGTGGCCCTCAAG 236
Db 97 GCCTTTTCCGAAGTGGTTTAGCTGAAGAGAAAGCAACTGGCAAGCTCTTTGCTGTGAAG 156

QY 237 TGCATTTCCCAAGAAAGCACTTCGGGGCAAGGAGGCCCTTGGTGGAGAAATGAGATCGCGGTA 296
Db 157 TGTATCCCTAAGAAAGGCGCTGAAGGGCAAGGAAAGCAGCATAGAGAATGAGATAGCCGTC 216

QY 297 CTTGCGCAGAATCAGCCATCCCAACATTTGTGGCTCTGGAGGACGTCCATGAGAGTCTTCT 356
Db 217 CTGAGAAAGATTAAAGCATGAAATAATTGTTGCCCTGGAAGACATTTATGAAAGCCCAAAT 276

QY 357 CATCTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAACCTGTTTGACCGCATCATGGAG 416
Db 277 CACCTGTACTTGGTCTATGAGCTGGTGTCCGGTGGAGAGCTGTTTGACCGGATAGTGGAG 336

QY 417 CGGGGCTCCTACACAGAGAAGGACGCCAGCCACCTTGTAGGGCAGGTCTTGGCGCTGTC 476
Db 337 AAGGGGTTTATACAGAGAAGGATGCCAGCACTCTGATCCGCCAAAGTCTTTGGACGCCGTG 396

QY 477 TCCTACCTTCATAGCCTGGGATCGTGCACCGGACCTCAAGCCTGAAAAACCTCTCTAT 536
Db 397 TACTATCTCCACAGAATGGGCATCGTCCACAGAGACCTCAAGCCCGAAAAATCTCTGTAC 456

QY 537 GCCACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTGGCCTGTGCCAAATACAA 596

Db 457 TACAGTCAAGATGAGGAGTCCAAAATAATGATCAGTGACTTTGGATTGTCAAAAATGGAG 516  
QY 597 G---CTGGCAACATGCTAGGCACAGCCTGTGGGACCCACAGGATATGTGGCCCCACAGAGTCC 653  
Db 517 GGCAAAGGAGATGTGATGTCCACTGCCCTGTGGAATCCAGGCTATGTGGTCTCCTGAAGTC 576  
QY 654 CTGGAGCAGAAACCTACGGGAAGGCCGTAGATGTGTGGGCCCTTGGGTGTCAATCTCCTAC 713  
Db 577 CTCGCCCAGAAACCTTACAGCAAAAGCCGTGACTGCTGGTCCATCGGAGTGATTGCCTAC 636  
QY 714 ATCCTGCTGTGGGTACCCCCCCTTCTATGATGAGAGCGATCCTGAACTCTTCAGCCAG 773  
Db 637 ATCTTGCTCTGGGCTACCCCTCCTTTTATGATGAAAAATGACTCCAAGCTCTTTGAGCAG 696  
QY 774 ATTCTGAGGCCAGCTATGAGTTTGACTCCCCCTTTTGGGATGACATCTCAGAAATCAGCC 833  
Db 697 ATCCTCAAGCGGAATATGAGTTTGACTCTCCCTACTGGGATGACATCTCCGACTCTGCA 756  
QY 834 AAAGACTTCATTCGCCACACTTCTGGAACGTGATCCCCAGAAAGGTTACCTGCCAGCAG 893  
Db 757 AAAGACTTCATTCGGAACCTGATGGAGAAGGACCCGGAATAAAGATACACGTGTGAGCAG 816  
QY 894 GCCCTACAGCATCTTTGGATCTCTGGGATGACGCTTCGATAGGGACATCCTGGGTTCT 953  
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QY 954 GTCAGTGAGCAGATCCAGAAGAATTTTGGCAGGACCCACTGGAAGCGTGCATTCAATGCC 1013  
Db 877 GTCAGCGCCAGATCCGGAAAAAATTTGGCAAGAGCAAAATGGAGACAAGCATTTAATGCC 936  
QY 1014 ACATCATTCCTACGTACATCCGTAAGCT 1042  
Db 937 ACGGCCGTCTGAGACATATGAGAAAACT 965

RESULT 12  
US-10-446-175-1  
; Sequence 1, Application US/10446175  
; Patent No. 6806073  
; GENERAL INFORMATION:  
; APPLICANT: Donoho, Greg  
; APPLICANT: Scoville, John  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Abuin, Alejandro  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: No. 6806073el Human Kinase Proteins and  
; FILE REFERENCE: LEX-0103-USA  
; CURRENT APPLICATION NUMBER: US/10/446,175  
; CURRENT FILING DATE: 2003-05-27  
; PRIOR APPLICATION NUMBER: US/09/733,388  
; PRIOR FILING DATE: 2000-12-07  
; PRIOR APPLICATION NUMBER: US 60/169,428  
; PRIOR FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1158  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-446-175-1  
Query Match 28.1%; Score 436.2; DB 4; Length 1158;  
Best Local Similarity 67.6%; Pred. No. 4.8e-123;  
Matches 628; Conservative 0; Mismatches 298; Indels 3; Gaps 1;  
QY 117 AAGAAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAAAGCTGGGCTCGGGT 176  
Db 37 AAAAAAGCAAGCTGAAGACATCAAGAAGATCTTCGAGTTCAAAGAGACCCCTCGGAACCGGG 96

QY 177 GCCTTCTCTGAGGTGATGCTGCCCAGGAAAGGGGCTCTGCTCATCTTGTGGCCCTCAAG 236  
Db 97 GCCTTTTCCGAAGTGGTTTAGCTGAAGAGAAAGGCAACTGGCAAGCTCTTTGCTGTGAAG 156  
QY 237 TGCATTTCCCAAGAAAGCACITTCGGGGCAAGGAGGCCCTGTGTGGAGAATGAGATCGCGGTA 296  
Db 157 TGTATCCCTAAGAAAGGCGCTGAAGGCAAGGAAAGCAGCATAGAGAATGAGATAGCCGTC 216  
QY 297 CTTCGCAGAAATCAGCCATCCCAACATTGTGTGGCTCTGGAGGACGTCATGAGAGTCCCTTCT 356  
Db 217 CTGAGAAAGATTAAAGCATGAAATATATGTGTCCTGGAAGACATTTATGAAAGCCCAAT 276  
QY 357 CATCTCTACTTGGCCATGGAGCTGGTAAACAGGTGGTGAACTGTTTGACCGCATCATGGAG 416  
Db 277 CACCTGTACTTGGTCAATGCAGCTGGTGTCCGGTGGAGAGCTGTTTGACCGGATAGTGGAG 336  
QY 417 CGGGGCTCTTACACAGAGAAGGACGCCAGCCAGCCACCTTGTAGGGCAGGTCTTGGCGCTGTC 476  
Db 337 AAGGGGTTTATACAGAGAAGGATGCCAGCACCTCTGATCCGCCAAGTCTTGGACGCCGTG 396  
QY 477 TCCTACTTTCATAGCCTGGGCATCGTGCACCGGGACCTCAAGCCTGAAAAACCTCCTCTAT 536  
Db 397 TACTATCTCCACAGAATGGGCATCGTCCACAGAGACCTCAAGCCCGAAAAATCTCTGTAC 456  
QY 537 GCCACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTTGGSCCTGTCCAAAATACAA 596  
Db 457 TACAGTCAAGATGAGGAGTCCAAAATAATGATCAGTGACTTTGGATTGTCAAAAATGGAG 516  
QY 597 G---CTGGCAACATGCTAGGCACAGCCTGTGGGACCCAGGATATGTGGCCCCAGAGCTC 653  
Db 517 GGCAAAAGGAGATGTGATGTCCACTGCCTGTGGAACTCCAGGCTATGTGCTCTTGAAGTC 576  
QY 654 CTGGAGCAGAAAAACCTTACGGGAAGGCCGTAGATGTGTGGCCCTTGGGTGTCTCTCTAC 713  
Db 577 CTCGCCCAGAAAACTTACAGCAAAAGCCGTGACTGCTGGTCCATCGGAGTGTGCCTAC 636  
QY 714 ATCCTGCTGTGGGTACCCCCCTTCTATGATGAGAGCGATCCTGAACTCTTCAGCCAG 773  
Db 637 ATCTTGCTCTCGGGCTACCCCTCCTTTTATGATGAAAAATGACTCCCAAGCTCTTTGAGCAG 696  
QY 774 ATTCTGAGGCCAGCTATGAGTTTGACTCCCCCTTTTGGGATGACATCTCAGAATCAGCC 833  
Db 697 ATCCTCAAGCGGGAATATGAGTTTGACTCTCCCTACTGGGATGACATCTCGACTCTGCA 756  
QY 834 AAAGACTTCATTCGCCACCTTCTGGAACGTGATCCCCAGAAAGGTTACCTGCCAGCAG 893  
Db 757 AAAGACTTCATTCGGAACCTGATGGAGAAGGACCCGGAATAAAGATACACGTGTGAGCAG 816  
QY 894 GCCCTACAGCATCTTTGGATCTCTGGGATGACGCTTCGATAGGGACATCCTGGGTTCT 953  
Db 817 GCAGCTCGGCACCCCATGGATCGTGGTGACACAGCCCTCAACAAAACATCCACGAGTCC 876  
QY 954 GTCAGTGAGCAGATCCAGAAGAATTTTGGCAGGACCCACTGGAAGCGTGCATTCAATGCC 1013  
Db 877 GTCAGCGCCAGATCCGGAAAAAATTTGGCAAGAGCAAAATGGAGACAAGCATTTAATGCC 936  
QY 1014 ACATCATTCCTACGTACATCCGTAAGCT 1042  
Db 937 ACGGCCGTCTGAGACATATGAGAAAACT 965

RESULT 13  
US-09-733-388-5  
; Sequence 5, Application US/09733388  
; Patent No. 6602698  
; GENERAL INFORMATION:  
; APPLICANT: Donoho, Greg  
; APPLICANT: Scoville, John  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Abuin, Alejandro  
; APPLICANT: Sands, Arthur T.



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; TITLE OF INVENTION: No. 6602698el Human Kinase Proteins and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0103-USA
; CURRENT APPLICATION NUMBER: US/09/733,388
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,428
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1671
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-733-388-5

Query Match      28.1%; Score 436.2; DB 4; Length 1671;
Best Local Similarity 67.6%; Pred. No. 6.1e-123;
Matches 628; Conservative 0; Mismatches 298; Indels 3; Gaps 1;

QY 117 AAGAAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAAGCTGGGCTCGGTT 176
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QY 417 CGGGCTCTACACAGAGAAGGAGCCAGCCACTTGTAGGGCAGGTCTTGGCGTGTCT 476
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; Patent No. 6806073
; GENERAL INFORMATION:
; APPLICANT: Donoho, Greg
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Abuin, Alejandro
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. 6806073el Human Kinase Proteins and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0103-USA
; CURRENT APPLICATION NUMBER: US/10/446,175
; CURRENT FILING DATE: 2003-05-27
; PRIOR APPLICATION NUMBER: US/09/733,388
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,428
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 1671
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-446-175-5
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Query Match      28.1%; Score 436.2; DB 4; Length 1671;
Best Local Similarity 67.6%; Pred. No. 6.1e-123;
Matches 628; Conservative 0; Mismatches 298; Indels 3; Gaps 1;

QY 117 AAGAAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAAGCTGGGCTCGGTT 176
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
203 AAAAAGCAAGCTGAAGACATCAAGAAGATCTTCGAGTTCAAAGAGACCCTCGGAACCGGG 262
QY 177 GCCTTCTCTGAGGTGATGTGGCCAGGAAAGGGCTCTGCTCATCTTGTGGCCCTCAAG 236
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QY 297 CTTCGCAGAATCAGCCATCCCAACATTTGGGCTCTGGAGGACGTCCATGAGAGTCCTTCT 356
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383 CTGAGAAAGATTAAAGCATGAAATATTGTTGCCCTGGAAGACATTTATGAAAGCCCAAT 442
QY 357 CATCTCTACTTGGCCATGGAGCTGGTAAACAGGTGGTGAACCTTTGACCGCATCATGGAG 416
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
443 CACCTGTACTTGGTCATGCAGCTGGTGTCCGGTGGAGAGCTGTTGACCGGATAGTGGAG 502
QY 417 CGGGCTCTACACAGAGAAGGAGCCAGCCACTTGTAGGGCAGGTCTTGGCGTGTCT 476
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503 AAGGGTTTTTATACAGAGAAGGATGCCAGCACTCTGATCCGCCAAGTCTTTGGACGCCGTG 562
QY 477 TCCTACCTTCATAGCCTGGGCATCGTGACCCGGGACCTCAAGCCTGAAAACCTCCTCTAT 536
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563 TACTATCTCCACAGAATGGGCATCGTCCACAGAGACCTCAAGCCCGAAATCTCTTTGTAC 622
QY 537 GCCACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTGGCCTGTCCAAAATACAA 596
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Db      683 GGCAAAAGGAGATGTGATGTCCACTGCCTGTGGAATCCAGGCTATGTCGCTCCTGAAATC 742
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Qy      714 ATCCTGTGTGTGGGTACCCCCCTTCTATGATGAGAGCGATCCTGAACTCTTCAAGCCAG 773
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US-09-620-312D-526
; Sequence 526, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yunqing
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Dрманac, Radoje T.
; TITLE OF INVENTION: No. 6569662e1 Nucleic Acids and
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 784CIP2B
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt FL_genes Version 1.0
; SEQ ID NO 526
; LENGTH: 1733
; TYPE: DNA
; ORGANISM: Homo sapiens
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (215)..(1372)
US-09-620-312D-526

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Best Local Similarity 67.6%; Pred. No. 6.2e-123;
Matches 628; Conservative 0; Mismatches 298; Indels 3; Gaps 1;

Qy      117 AAGAAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAAAGTGGCTCGGGT 176
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SUMMARIES

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2	903.8	58.2	1452	17	US-10-425-114-26649 Sequence 26649, A
3	859	55.3	1584	17	US-10-302-172-205 Sequence 205, App
4	844.4	54.3	1282	10	US-09-769-970-12 Sequence 12, Appl
5	844.4	54.3	1282	17	US-10-305-720-953 Sequence 953, App
6	844.4	54.3	1282	18	US-10-656-598-5 Sequence 5, Appli
7	844.4	54.3	1282	18	US-10-643-795A-9 Sequence 9, Appli
8	844.4	54.3	1282	19	US-10-948-518-9 Sequence 9, Appli
9	544	35.0	641	18	US-10-656-598-15 Sequence 15, Appl
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11	500.8	32.2	1480	17	US-10-305-720-1454 Sequence 1454, Ap

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ALIGNMENTS

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; Sequence 5, Application US/09735138  
; Publication No. US20030176666A1  
; GENERAL INFORMATION:  
; APPLICANT: Sutcliffe, J. Gregor  
; Gautvik, Kaare M.  
; De Lecea, Luis  
; Bloom, Floyd E.  
; Danielson, Patria E.  
; Kilduff, T.S.  
; Gautvik, Vigdis T.  
; Foye, Pamela E.  
; TITLE OF INVENTION: Hypothalamus-Specific Polypeptides  
; NUMBER OF SEQUENCES: 15  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Olson & Hierl, Ltd.  
; STREET: 20 No. US20030176666A1th Wacker Drive, 36th Floor  
; CITY: Chicago  
; STATE: IL  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/735,138  
; FILING DATE: 12-Dec-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/023,220  
; FILING DATE: 02-AUG-1996

```

;
; ATTORNEY/AGENT INFORMATION:
; NAME: Talivaldis Cepuritis
; REGISTRATION NUMBER: 20,818
; REFERENCE/DOCKET NUMBER: TSRI 548.1 DIV.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-580-1180
; TELEFAX: 312-580-1189
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1458 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-735-138-5

      Query Match      81.2%; Score 1261.2; DB 10; Length 1458;
      Best Local Similarity 93.6%; Pred. No. 0;
      Matches 1348; Conservative 0; Mismatches 63; Indels 29; Gaps 2;

QY 99 GCAGACATGCTGCTGCTCAAGAAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGG 158
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Db 44 GCAGACATGCTGCTCAAGAAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGG 103

QY 159 GAGAAAGCTGGGCTCGGGTGCCCTTCTCTGAGGTGATGCTGGCCCAAGAAAGGGCTCTGCT 218
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 104 GAGAAAGCTGGGCTCGGGTGCCCTTCTCTGAGGTGATGCTGGCCCAAGAAAGGGCTCTGCT 163

QY 219 CATCTTGTGGCCCTCAAGTGCAATCCCAAGAAAGCACTTCGGGGCAAGAGGCCCTGGTG 278
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 164 CATCTTGTGGCCCTCAAGTGCAATCCCAAGAAAGCACTTCGGGGCAAGAGGCCCTGGTG 223

QY 279 GAGAAATGAGATCGCGGTACTTCGCAGAAATCAGCCATCCCAACATTGTGGCTCTGGAGGAC 338
   |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 224 GAGAAATGAGATCGCAGTACTCCGCAGGATTAGCCACCCCAACATTGTGGCTCTGGAGGAC 283

QY 339 GTCCATGAGAGTCCTTCTCATCTCTACTTGGCCATGGAGCTGGTAAACAGGTGGTGAAC TG 398
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 284 GTCCACGAGAGCCCTTCCCATCTCTACTTGGCCATGGAGCTGGTAAACAGGTGGTGAAC TG 343

QY 399 TTTGACCGCATCATGGAGCGGGCTCCTACACAGAGAAGGACGCCAGCCACCTTGTAGGG 458
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 344 TTTGACCGAATCATGGAGCGGGCTCCTACACAGAGAAGGATCGAGGCCACCTTGTAGGG 403

QY 459 CAGGTCTTGGCGCTGTCTCCTACCTTCATPAGCCTGGGCATCGTGACCCGGACCTCAAG 518
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 404 CAGGTCTTGGTGTGTCTCCTACCTTCATAGCCTGGGCATCGTGACCCGGGACCTCAAG 463

QY 519 CCTGAAAACCTCCTCTATGCCACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTT 578
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Db 464 CCTGAAAACCTCCTCTATGCCACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTT 523

QY 579 GGCCTGTCCAAAATACAAGCTGGCAACATGCTAGGCACAGCCTGTGGACCCCAAGGATAT 638
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Db 524 GGCCTGTCCAAAATTCAAGCTGGCAACATGCTAGGCACAGCCTGTGGACCCCAAGGATAT 583

QY 639 GTGGCCCCAGAGCTCCTGGAGCAGAAACCTTACGGGAAGGCCGTAGATGTGTGGGCCCTG 698
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Db 584 GTGGCCCCAGAGCTCCTGGAGCAGAAACCTACGGGAAGGCCGTAGATGTGTGGGCCCTG 643

QY 699 GGTGTATCTCTACATCCTGTGTGGGTACCCCCCTTCTATGATGAGAGCGATCCT 758
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Db 644 GGTGTATCTCTACATCCTGTGTGGGTACCCCCCTTCTATGATGAGAGCGATCCT 703

QY 759 GAACTCTTCAGCCAGATTCTGAGGGCCAGCTATGAGTTTGACTCCCCCTTTTGGGATGAC 818
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 704 GAACTCTTCAGCCAGATTCTGAGGGCCAGCTACGAGTTTGACTCTCCCTTTTGGGATGAC 763

QY 819 ATCTCAGAATCAGCCAAAGACTTCAATTCGCCACCTTCTTGGAACGTGATCCCAAGAGG 878
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Db 764 ATCTCAGAATCAGCCAAAGACTTCATTCGGCACCTTCTGGAACTGATCCCCAGAAGAGG 823
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QY 879 TTCACCTGCCAGCAGGCCCTACAGCATCTTTGGATCTCTGGGATGCAGCCTTCGATAGG 938
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 824 TTCACCTGCCAAACAGGCCCTTACAGCATCTCTGGATCTCTGGGATGCAGCCTTGGACAGG 883
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 939 GACATCCTGGGTTCTGTCACTGAGCAGATCCAGAAGAAATTTGCCAGGACCCACTGGAAG 998
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 884 GACATCCTAGGTTCTGTCACTGAGCAGATCCAGAAGAAATTTGCCAGGACCCACTGGAAG 943
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 999 CGTGCAATTCAATGCCACATCATTCCTACGTACATCCGTACATGCCACCCAGCCCTTGGGACTAGC 1058
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 944 CGTGCAATTCAATGCCACATCATTCCTACGTACATCCGTACATGCCAGAGAGCCAGAG 1003
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1059 GGTGAGGAGGCCCTCCAGGCAGTGTATGACCCGTATGACCCATAGCCACCCAGCCCTTGGGACTAGC 1118
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1004 GGTGAGGAGGCCCTCCAGGCAGGATGACCCGTACAGCCACCCAGGCCCTTGGGACTAGC 1063
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1119 CAGTCCCCCAAAGTGGTGAACCCAGGTAGATGCCAAGGAAGGCCAAGTGGAAGTACTGCC 1178
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1064 CAGTCCCCCAAAGTGGTGACAAACAGGTGGATGCCAAGGAAGGCCAAGTGGAAGTACTGCC 1123
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1179 GGTTTTTCTTCTCCAGCCCTTTTGGTCTCTTTCTGGATCCTTGTCTCCAGACTGGC 1238
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1124 AGCTTTTCTTCTCCAGCCCTTTTGATCTCCTTCCCTGATCCTTGTCTCCCGGACTGGC 1183
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1239 CTCTGCTGGAAGTCTGAGAC--TGGGTGTGATGCATGGCATGGGTACGGGCTTCCC 1296
   ||||||| ||||||| ||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1184 CTCTGTTGGAAGTCCAAGACCCGTGGTGTGATGCATGGCATGGGTATGGGCTTCCC 1243
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1297 CAGTATGTCCCCCAGCCCTCTATTCTTACCTATGGTGGAGGCTCCCTTTCCCATGTGCTG 1356
   ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1244 AAGTATGTCCCC-----AGCCTCTGTCTTTGTTGCTG 1276
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1357 CCACCTCTATGGAAACTGAGAGGTGTTCAAAGTGGACTTGGAGCCATCCTTCTCTGC 1416
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1277 CCACCTCTATGGAAACTGAGAGGTATTCAAAATGGATTGGGGGCCATCCTTCTCTGC 1336
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1417 ACCTTGACGAACACATGCAATGTGTGGTGTCTGTGCTTTGCTGACTGTGGTGGTCC 1476
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1337 ACCTTGACGCACATATGCAATGGTGGTGTCTGTGCTTTGCTGACTGTGGTGGTCC 1396
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
QY 1477 TGCTTGTGTGTGGCCCTTTAGTTCCCTCTTCTTAACCAATAAAGACAAACAGAACCA 1536
   ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 1397 TGCTTGTGTGTAGCCCTTTAGTTCCCTCTTCTTCCAACCAATAAAGACAAACAGAACAA 1456
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RESULT 2
US-10-425-114-26649
; Sequence 26649, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 26649
; LENGTH: 1452
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4653-002-F12_FLI
US-10-425-114-26649
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Query Match		58.2%;	Score 903.8;	DB 17;	Length 1452;
Best Local Similarity		79.9%;	Pred. No. 1.1e-269;		
Matches 1131;		Conservative 0;	Mismatches 267;	Indels 17;	Gaps 5;
QY	94	GGGTGCGAGACATGCTGTCTCAAGAAACAGACGAGGACATCAGCAGTGTCTATGAGA	153		
Db	6	GGGAGCGGACATGCTGTCTGAAGAAACACACGAGGACATCAGCAGCGTCTACGAGA	65		
QY	154	TCCGGGAGAAAGCTGGGTCGGGTGCCTTCTCTGAGGTGATGCTGGCCCAAGAAAGGGCT	213		
Db	66	TCCGCGAGAGGCTCGGCTCGGGTGCCTTCTCCGAGGTGCTGTGCCCAAGAGCGGGGCT	125		
QY	214	CTGCTCATCTTGTGGCCCTCAAGTGCATTCCTCAAGAAAGCACTTCGGGGCAAGAGGCC	273		
Db	126	CCGCACACCTCGTGGCCCTCAAGTGCATCCCCAAGAAAGGCCCTCCGGGGCAAGAGGCC	185		
QY	274	TGGTGGAGAAATGAGATCGGGTACTTCGCAGAAATCAGGCATCCCCAACATTTGGCTCTGG	333		
Db	186	TGGTGGAGAAACGAGATCGCAGTGTCTCCGTAGGATCAGTCAACCCCAACATCGTCGCTCTGG	245		
QY	334	AGGACGTCCATGAGAGTCCCTTCTCATCTCTACTTTGSCCATGGAGCTGGTAACAGTGGTG	393		
Db	246	AGGATGTCCACGAGAGCCCTTCCCACCTCTACCTGGCCATGGAACTGGTGACGGGTGGCG	305		
QY	394	AACTGTTTGACCGCATCATGGAGCGGGGCTCCTACACAGAGAAGGACGCCAGCACCTTG	453		
Db	306	AGCTGTTTGACCGCATCATGGAGCGCGGCTCCTACACAGAGAAGGATGCCAGCCATCTGG	365		
QY	454	TAGGGCAGGTCTTGGCGTGTCTCTACCTTCATAGCCTGGGCATCGTGCACCGGGACC	513		
Db	366	TGGGTGAGTCTTGGGCGGTCTCTACCTGTCACAGCCTGGGGATCGTGCACCGGGACC	425		
QY	514	TCAAGCCTGAAAACCTCTCTATGCCCACACCTTTTGAGGACTCCAAGATCATGGTCTCTG	573		
Db	426	TCAAGCCCGAAAACCTCTGTATGCCAGCCCTTTGAGGACTCGAAGATCATGTTCTCTG	485		
QY	574	ACTTTGGCCTGTCCAAAATACAAGCTGGCAACATGTAGGCACAGCCTGTGGGACCCCG	633		
Db	486	ACTTTGGACTCTCCAAAATCCAGGCTGGGAACATGCTAGGCACCGCTGTGGGACCCCTG	545		
QY	634	GATATGTGGCCCCAGAGTCTCTGGAGCAGAAACCCCTACGGGAAGCCGTAGTGTGGG	693		
Db	546	GATATGTGGCCCCAGAGTCTTTGGAGCAGAAACCCCTACGGGAAGCCGTAGTGTGGG	605		
QY	694	CCCTGGGTGTATCTCTACATCTCTGTGTGGGTACCCCTTCTATATGATGAGAGCG	753		
Db	606	CCCTGGGCGTATCTCTACATCTCTGTGTGGGTACCCCTTCTACGACGAGAGCG	665		
QY	754	ATCCTGAACCTCTTCAGCCAGATTTCTGAGGGCCAGCTATGAGTTTGACTCCCTTTTGGG	813		
Db	666	ACCCTGAGCTCTTCAGCCAGATCTCTGAGGGCCAGCTATGAGTTTGACTCTCTTCTTGGG	725		
QY	814	ATGACATCTCAGAAATCAGCCAAAGACTTCATTCGCCACCTTCTGGAACGTGATCCCCAGA	873		
Db	726	ATGACATCTCAGAAATCAGCCAAAGACTTCATCCGGCACCTTCTGGAGCGAGACCCCCAGA	785		
QY	874	AGAGGTTACCTGCCAGAGGCCCTTACAGCATCTTTGGATCTCTGGGGATGCAGCCTTCG	933		
Db	786	AGAGGTTACCTGCCACAGGCCCTTGGGCACCTTTGGATCTCTGGGACACAGCCTTCG	845		
QY	934	ATAGGGACATCCTGGGTTCTGTCAGTGAGCAGATCCAGAAAGAAATTTTGCCAGGACCCACT	993		
Db	846	ACAGGGACATCTTAGGCTCTGTCAGTGAGCAGATCCGGAAGAACTTTGCTCGGACACACT	905		
QY	994	GGAAGCGTGCATTCATATGCCACATCATTCCTACGTACATCCGTAAGCTGGGACAAAGCC	1053		
Db	906	GGAAGCGAGCCTTCATATGCCACCTCTGTTCTCTGCGCCACATCCGGAAGCTGGGGCAGATCC	965		
QY	1054	CAGAGGGTGAGGAGGCCCTCCAGGCAGTGTATGACCCGTATAGCCACCCAGG-CCTTGGG	1112		
Db	966	CAGAGGGCGAGGGGCTCTGAGCAGGGCATGGCCCGCCACAGCCACTCAGGCCCTCCGT	1025		
QY	1113	ACTAGCCAGTCCCCCAAGTGGTGAANAACAGGTAGATGCCAAGGAAGGCCAAGTGGACTG	1172		

Db	1026	GCTGGCCAGCCCCCAAGTGGTGATGCCAGGCAGATGCC----	1081	
QY	1173	ACTCCCGGTTTTTCTTCCCTCCAGCCCTTTTGGTCTCTTTCTCTGGATCCTTGTCTCTCCAG	1232	
Db	1082	ACCCCAGATTTCTTCCCTTGGATGCTTTCGGTCCCCTCCCCCAACCCCTCCCCCTGGG	1141	
QY	1233	ACTGGCCTCTGCTGGAAAGTCTGA-GACTGGGTGTGATGCATGGCACTAGGGT----	1287	
Db	1142	GCTGGCCTCTGCTGGATTTTGAGATTTGAGGGTGTGGCGCATGGCGCTGGGGTTGGAATG	1201	
QY	1288	GGGCTTCCCCAGTATGTCCCCCAGCCTCTATTCTTACCTATGGTGGAGGCTCCCTTTCC	1347	
Db	1202	GGGACACCCCAAGTCTGTCCCCCAGGCTCTGCCCTGCCTGGGGCAGTGGCTCCCCCTCCC	1261	
QY	1348	ATGTCGCTGCCACCCCTCTATGGAAACTGAGGAGGTGTTCAAAAGTGGACTTTGGGAGCCAT	1407	
Db	1262	TGTTGCCTCTCCCGCCCTGCCCTCCCGCCCGCCCGCCCAAGCCGAGGGGTGCTGGCAGG	1321	
QY	1408	CCTTCCTGCACCTTGCACGAACACATGCATTTGTGGCTGTTCTGTGCTTTGCTGACTGT	1467	
Db	1322	CGGGCC-----TCAGGGGCTGTCTTTCTCTGCACGGCTGTTGTGCTTCGCTGAGTGT	1374	
QY	1468	GGTGGTCTGCTTGTGTTGTGGCCCTTTAGTTTC	1502	
Db	1375	GGTGGTCTGCTTGTGTCATGGTCAATGGCCTTCC	1409	
RESULT 3				
US-10-302-172-205				
; Sequence 205, Application US/10302172				
; Publication No. US20040053250A1				
; GENERAL INFORMATION:				
; APPLICANT: Tang, Y. Tom				
; APPLICANT: Xue, Aidong J.				
; APPLICANT: Drmanac, Radoje T.				
; TITLE OF INVENTION: No. US20040053250A1e1 Arginine-rich Protein-like Nucleic				
; TITLE OF INVENTION: Polypeptides				
; FILE REFERENCE: 803 1CNCP				
; CURRENT APPLICATION NUMBER: US/10/302,172				
; CURRENT FILING DATE: 2002-11-21				
; PRIOR APPLICATION NUMBER: US 10/225,251				
; PRIOR FILING DATE: 2002-08-20				
; PRIOR APPLICATION NUMBER: PCT US02/05095				
; PRIOR FILING DATE: 2002-03-05				
; PRIOR APPLICATION NUMBER: US 09/799,451				
; PRIOR FILING DATE: 2001-03-05				
; NUMBER OF SEQ ID NOS: 950				
; SOFTWARE: pt_FL_genes Version 2.0				
; SEQ ID NO 205				
; LENGTH: 1584				
; TYPE: DNA				
; ORGANISM: Homo sapiens				
; FEATURE:				
; NAME/KEY: CDS				
; LOCATION: (51)..(1166)				
US-10-302-172-205				
Query Match 55.3%; Score 859; DB 17; Length 1584;				
Best Local Similarity 78.7%; Pred. No. 9.7e-256;				
Matches 1098; Conservative 0; Mismatches 270; Indels 27; Gaps 5;				
QY	168	GGCTCGGGTGCCTTCTCTGAGGTGATGCTGGCCAGGAAAGGGGCTCTGCTCATCTTGTG	227	
Db	201	GGCAGGGTGCCTTCTCCGAGGTGGTGTGGCTGGCCAGGAGCGGGGCTCCGCACACCTCGTG	260	
QY	228	GCCCTCAAGTGCATTTCCCAAGAAAGCACTTCGGGGCAAGGAGGCCCTGGTGGAGATGAG	287	
Db	261	GCCCTCAAGTGCATTTCCCAAGAAAGGCCCTCCGGGGCAAGGAGGCCCTGGTGGAGAACGAG	320	
QY	288	ATCGCGGTACTTCGAGAAATCAGCCATCCCAACATTGTGGCTCTGGAGGACGTCATGAG	347	
Db	321	ATCGCAGTGTCCGTAGGATCAGTCACCCCAACATCGTCTGCTCTGGAGGATGTCCACGAG	380	



Db 197 AAACATGCTGCTGAAGAAACACACGGAGGACATCAGACGCTCTACGAGATCCGCGA 256

QY 161 GAAGCTGGGCTCGGGTGCTTCTCTGAGGTGATGCTGGCCCCAGGAAAGGGGCTCTGCTCA 220

Db 257 GAGGCTCGGCTCGGGTGCTTCTCCGAGGTGGTGGCCCCAGGACGGGGCTCCGCACA 316

QY 221 TCTTGTGGCCCTCAAGTGCATTTCCCAAGAAACACTTCGGGGCAAGGAGGCCCTGGTGA 280

Db 317 CCTCGTGGCCCTCAAGTGCATTTCCCAAGAAAGGCCCTCCGGGGCAAGGAGGCCCTGGTGA 376

QY 281 GAATGAGATCGGGTACTTCGCAGAAATCAGCCATCCAAACATTTGTGGCTCTGAGGACGT 340

Db 377 GAACGAGATCGCAGTGTCTCGTAGGATCAGTACCCCAACATCGTCGCTCTGGAGGATGT 436

QY 341 CCATGAGAGTCTTCTCATCTCTACTTTGGCCATGGAGCTGGTAACAGGTGGTGAATGTT 400

Db 437 CCACGAGAGCCCTTCCCACTCTACCTGGCCATGGAATGGTGACGGGTGGCGAGCTGTT 496

QY 401 TGACCGCATCATGGAGCGGGCTCCTACACAGAGAGAGACGCCACCTTTGTAGGGCA 460

Db 497 TGACCGCATCATGGAGCGGGCTCCTACACAGAGAGGATGCCAGCCATCTGTGGGTCA 556

QY 461 GGTCTTGGCGCTGTCTCTACCTTCTATAGCTTGGCATCGTGACCGGGACCTCAAGCC 520

Db 557 GGTCTTGGCGCGCTCTCTACCTGCACAGCCTGGGATCGTGACCGGGACCTCAAGCC 616

QY 521 TGAAAACTCTCTATGCCACACCTTTTGGAGACTTCAAGATCATGGTCTCTGACTTTGG 580

Db 617 CGAAAACTCTGTATGCCACGCGCTTTGAGGACTCGAAGATCATGGTCTCTGACTTTGG 676

QY 581 CCTGTCCAAAATACAAAGTGGCAACATGCTAGGCACAGCCTGTGGACCCCAAGATATGT 640

Db 677 ACTCTCCAAAATCCAGGCTGGGAACATGTAGGCACCGCTGTGGACCCCTGGATATGT 736

QY 641 GGCCCCAGAGCTCCTGGAGCAGAAACCTTACGGGAAGGCCGTAGATGTGTGGSCCTGGG 700

Db 737 GGCCCCAGAGCTCTTGGAGCAGAAACCTTACGGGAAGGCCGTAGATGTGTGGSCCTGGG 796

QY 701 TGTCTCTCTACATCCTGTGTGTGGGTACCCCTCTCTATGATGAGAGCGATCTCTGA 760

Db 797 CGTCATCTCTACATCCTGTGTGTGGGTACCCCTCTCTACGACGAGAGCACCTTGA 856

QY 761 ACTCTTACGCCAGATCTGAGGGCCAGCTATGAGTTGACTCCCTTTTGGGATGACAT 820

Db 857 GCTCTTACGCCAGATCCTGAGGGCCAGCTATGAGTTGACTNTCTTTCTGGGATGACAT 916

QY 821 CTCAGAATCAGCCAAAGACTTCAATTCGCCACCTTCTGGAACGTGATCCCCAGAGAGGTT 880

Db 917 CTCAGAATCAGGCCAAAGACTTTATTCGGCACCTTCTGGAGCGAGACCTTCAGAGAGGTT 976

QY 881 CACCTGCCAGCAGGCCCTTACAGCATCTTTGGATCTCTGGGGATGCAGCCCTTCATAGGGA 940

Db 977 CACCTGCCAACAGGCCCTTGGGGACCTTTGGATCTTTGGGACACAGGCTTTGGCAGGGA 1036

QY 941 CATCCTGGGTTCTGTCAGTGAGCAGATCCAGAAATTTTGGCAGGACCCACTGGAAGCG 1000

Db 1037 CATCTTAGGGTTTGTCAGTGAGCAGATCCGGAAGAACTTTGTCTTGACACACTGGAAGCG 1096

QY 1001 TGCATTCAATGCCACATCATCTTACGTACATCCGTAAGCTGGGACAAAGCCAGAGGG 1060

Db 1097 AGCCTTCAATGCCACCTTGTCTCTGGCCACATCCCGAAGCTGGGGCAGATCCAGAGGG 1156

QY 1061 TGAGGAGGCCCTCCAGGCAAGTATGACCCGTATAGCCACCCAGGCCCTTGGGACTAGCCA 1120

Db 1157 CGAGGGGGCTCTGAGCAGGGCATGGSCCGNCACAGCCACTNAGGCCCTTCGTGTGGCCA 1216

QY 1121 GTCCCCCAAGTGGTGAACCAAGGTAGATGCCAAGGAAGGCCAAGTGGACTGACTCCCGG 1180

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QY 1181 TTTTCTTTTC 1190

Db 1273 ATTNCTTNC 1282

RESULT 5

US-10-305-720-953  
; Sequence 953, Application US/10305720  
; Publication No. US20040010136A1  
; GENERAL INFORMATION:

; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.

; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression

; FILE REFERENCE: PA-0002-1 CON

; CURRENT APPLICATION NUMBER: US/10/305,720

; CURRENT FILING DATE: 2002-11-26

; PRIOR APPLICATION NUMBER: 09/016,434

; PRIOR FILING DATE: 1998-01-30

; NUMBER OF SEQ ID NOS: 1490

; SOFTWARE: PERL Program

; SEQ ID NO 953

; LENGTH: 1282

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Incyte ID No. US20040010136A1 827431

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1) ... (1282)

; OTHER INFORMATION: a, t, c, g, or other

US-10-305-720-953

Query Match 54.3%; Score 844.4; DB 17; Length 1282;  
Best Local Similarity 86.2%; Pred. No. 3.1e-251;  
Matches 940; Conservative 1; Mismatches 145; Indels 4; Gaps 1;

QY 101 AGACATGCTGCTCAAGAAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGGGA 160

Db 197 AAACATGCTGCTGAAGAAACACACGGAGGACATCAGCAGCTCTACGAGATCCGCGA 256

QY 161 GAAGCTGGGCTCGGTGCTTCTCTGAGGTGATGCTGGCCCCAGGAAAGGGCTCTGCTCA 220

Db 257 GAGGCTCGGCTCGGTGCTTCTCCGAGGTGGTGGCCCCAGGAGCGGGCTCCGCACA 316

QY 221 TCTTGTGGCCCTCAAGTGCATTTCCCAAGAAAGCACTTCGGGGCAAGGAGGCCCTGCTGGA 280

Db 317 CCTGTGGCCCTCAAGTGCATTTCCCAAGAAAGGCCCTTCGGGGCAAGGAGGCCCTGCTGGA 376

QY 281 GAATGAGATCGCGGTACTTCGCAGAAATCAGCCATCCCAACATTTGTGGCTCTGGAGGACGT 340

Db 377 GAACGAGATCGCAGTGTCTCGTAGGATCAGTACCCCAACATCGTCGCTCTGGAGGATGT 436

QY 341 CCATGAGAGTCTTCTCATCTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAATGTT 400

Db 437 CCACGAGAGCCCTTCCCACTCTACCTGGCCATGGAATGGTGACGGGTGGCGAGCTGTT 496

QY 401 TGACCGCATCATGAGCGGGGCTCCTACACAGAGAGGACGCCAGCCACCTTTGTAGGGCA 460

Db 497 TGACCGCATCATGAGCGGGGCTCCTACACAGAGAGGATGCCAGCCATCTGTGGTGGTCA 556

QY 461 GGTCTTGGCGCTGTCTCTTACCTTTCATAGCCCTGGGCATCGTGACCCGGGACCTCAAGCC 520

Db 557 GGTCTTGGCGCGCTCTCTTACCTTGACAGCCCTGGGGATCGTGACCCGGGACCTCAAGCC 616

QY 521 TGAAAACTCTCTATGCCACACCTTTTGGAGACTCCAAGATCATGGTCTCTGACTTTGG 580

Db 617 CGAAAACTCTCTATGTCACCGCCCTTTTGGAGACTCGAAGATCATGGTCTCTGACTTTGG 676

QY 581 CCTGTCCAAAATACAAAGCTGGCAACATGCTAGGCACAGCCTGTGGGACCCCAAGATATGT 640

Db 677 ACTCTCCAAAATCCAGGCTGGGAACATGCTAGGCACCGCTGTGGGACCCCTGGATATGT 736

QY 641 GGCCCCAGAGCTCCTGGAGCAGAAACCTTACGGGAAGGCCGTAGATGTGTGGSCCTGGG 700

Db 737 GGCCCCAGAGCTCTTGGAGCAGAAACCTTACGGGAAGGCCGTAGATGTGTGGSCCTGGG 796



QY 701 TGTCACTCCTACATCCTGCTGTGTGGGTACCCCCCTTCTATGATGAGAGCGATCCTGA 760  
Db |||||  
797 CGTCATCTCCTACATCCTGCTGTGTGGGTACCCCCCTTCTACGACGAGAGCGACCCCTGA 856  
QY 761 ACTCTTCAGGCAGATTCTGAGGGCCAGCTATGAGTTTGACTCCCCCTTTTGGGATGACAT 820  
Db |||||  
857 GCTCTTCAGCCAGATCCTGAGGGCCAGCTATGAGTTTGACTNTCCTTTCTGGGATGACAT 916  
QY 821 CTCAGAATCAGCCAAAGACTTTCATTTCGCCACCTTCTGGAACTGTGAACTGCCAGAAGAGGTT 880  
Db |||||  
917 CTCAGAATCAGGCAAAAGACTTTATTTCGGCACCTTCTGGAGCGAGACCTTCAGAAGAGGTT 976  
QY 881 CACCTGCCAGCAGGCCCTACAGCATCTTTGGATCTCTGGGATGCGAGCCTTCGATAGGGA 940  
Db |||||  
977 CACCTGCCAACAGGCCCTTGGGACCTTTGGATCTTTGGGACACAGGCTTTGGCAGGGA 1036  
QY 941 CATCCTGGGTTCTGTCAGTGAGCAGATCCAGAAAGAAATTTTGGCAGGACCCACTGGAAGCG 1000  
Db |||||  
1037 CATCTTAGGGTTGTCAGTGAGCAGATCCGGAAGAACTTTTGCTTGGACACACTGGAAGCG 1096  
QY 1001 TGCATTCAATGCCACATCATCTCCTACGTCATCCGTAAGCTGGGACAAAGCCAGAGGG 1060  
Db |||||  
1097 AGCCTTCAATGCCACCTTGTTCCTGCGCCACATCCGGAAGCTGGGGCAGATCCCAGAGGG 1156  
QY 1061 TGAGGAGGCCCTCAGGCAGTGTATGACCCGTATAGCCACCCAGGCCCTTGGGACTAGCCA 1120  
Db |||||  
1157 CGAGGGGGCCTCTGAGCAGGGCATGGSCCGNCACAGCCACTNAGGCCCTTCGTGTGGCCA 1216  
QY 1121 GTCCCCCAAGTGGTGA AAAAC CAGGTAGATGCCAAGGAAGGCCAAGTGGAGTCACTCCCGG 1180  
Db |||||  
1217 GCCCCCCAAGTGGTATGCCCAGGNAGATGCC----GAGGCCAAGTGGGANTGANCCCCAG 1272  
QY 1181 TTTTCTTTC 1190  
Db |||||  
1273 ATTNCTTNC 1282

RESULT 6

US-10-656-598-5  
; Sequence 5, Application US/10656598  
; Publication No. US20040229232A1  
; GENERAL INFORMATION:  
; APPLICANT: DAVID P. DAVIS  
; APPLICANT: FREDERIC J. DESAUVAGE  
; APPLICANT: WILLIAM I. WOOD  
; APPLICANT: ZEMIN ZHANG  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND  
; TITLE OF INVENTION: TREATMENT OF TUMOR  
; FILE REFERENCE: P1981R1P1-US  
; CURRENT APPLICATION NUMBER: US/10/656,598  
; CURRENT FILING DATE: 2003-09-05  
; PRIOR APPLICATION NUMBER: US 60/410,166  
; PRIOR FILING DATE: 2002-09-11  
; NUMBER OF SEQ ID NOS: 52  
; SEQ ID NO 5  
; LENGTH: 1282  
; TYPE: DNA  
; ORGANISM: Homo sapien  
; FEATURE:  
; NAME/KEY: Unsure  
; LOCATION: 898, 1187, 1198, 1241, 1262, 1266, 1277, 1281  
; OTHER INFORMATION: Unknown base  
US-10-656-598-5

Query Match 54.3%; Score 844.4; DB 18; Length 1282;  
Best Local Similarity 86.2%; Pred. No. 3.1e-251;  
Matches 940; Conservative 1; Mismatches 145; Indels 4; Gaps 1;  
QY 101 AGACATGCTGCTCAAGAAACAGACGAGGAGGACATCAGCAGTGTCTATGATCCGGGA 160  
Db |||||  
197 AAACATGCTGCTGAAGAAACACACGAGGAGGACATCAGCAGCGTCTACGAGATCCGGA 256  
QY 161 GAAGCTGGGCTCGGCTGCTTCTGTAGGTGATGCTGGCCCCAGGAAAGGGCTCTGCTCA 220

Db 257 GAGGCTCGGCTCGGCTGCCCTTCTCCGAGGTGGTGTGGCCCCAGGAGCGGGGCTCCGCACA 316  
QY 221 TCTTGTGGCCCTCAAGTGCAATCCCAAGAAAGCACTTCGGGGCAAGAGGCCCTTGGTGA 280  
Db |||||  
317 CCTGTGGCCCTCAAGTGCAATCCCAAGAAAGGCCCTCCGGGGCAAGAGGCCCTTGGTGA 376  
QY 281 GAATGAGATCGCGGTACTTCGCAGAATCAGCCATCCCAACATTTGTGGCTCTGGAGACGT 340  
Db |||||  
377 GAACGAGATCGCAGTGTCCGTAGGATCAGTACCCCCAACATCGTCGCTCTGGAGGATGT 436  
QY 341 CCATGAGATCCTTCTCATCTCTACTTGGCCCATGGAGCTGGTAACAGGTGGTGAACGTGT 400  
Db |||||  
437 CCACGAGAGCCCTTCCACCTCTACCTTGGCCATGGAACCTGGTGACGGGTGGCAGCTGT 496  
QY 401 TGACCGCATCATGGAGCGGGCTCCTACACAGAGAAGGACGCCAGCCACTTGTAGGGCA 460  
Db |||||  
497 TGACCGCATCATGGAGCGGGCTCCTACACAGAGAAGGATGCCAGCCATCTGTGTGGTCA 556  
QY 461 GGTCTTGGCGCTGTCTCCTACCTTATAGCCTTATAGCCTTGGCATCGTGACCCGGACCTCAAGCC 520  
Db |||||  
557 GGTCTTGGCGCGTCTCCTACCTGCAAGCCCTTGGAGACTCGAAGATCATGCTCTCTGACTTTGG 676  
QY 521 TGA AAACCTCCTATGCCACACCTTTTGGAGACTCCAAGATCATGCTCTCTGACTTTGG 580  
Db |||||  
617 CG AAACCTCCTGTATGCCAGCCCTTGGAGACTCGAAGATCATGCTCTCTGACTTTGG 676  
QY 581 CCTGTCCAAAATACAAGCTGGCAACATGCTTAGGCACAGCCCTGTGGGACCCAGGATATGT 640  
Db |||||  
677 ACTCTCCAAAATCCAGGCTGGGAACATGCTAGGCACCGCCTGTGGGACCCCTGGATATGT 736  
QY 641 GGCCCCAGAGCTCCTGGAGCAGAAACCCCTACGGGAAGGCCGCTAGATGTGTGGGCCCCTGGG 700  
Db |||||  
737 GGCCCCAGAGCTCTTGGAGCAGAAACCCCTACGGGAAGGCCGCTAGATGTGTGGGCCCCTGGG 796  
QY 701 TGTCACTCCTACATCCTGCTGTGTGGGTACCCCCCTTCTATGATGAGAGCGATCCTGA 760  
Db |||||  
797 CGTCATCTCCTACATCCTGCTGTGTGGGTACCCCCCTTCTACGACGAGAGCACCCCTGA 856  
QY 761 ACTCTTCAGCCAGATTTGAGGGCCAGCTATGAGTTTGACTCCCCCTTTTGGGATGACAT 820  
Db |||||  
857 GCTCTTCAGCCAGATCCTGAGGGCCAGCTATGAGTTTGACTNTCCTTCTGCGATGACAT 916  
QY 821 CTCAGAATCAGCCAAAGACTTCATTTCGCCACCTTCTGGAACGCTGATCCCCAGAAGAGGTT 880  
Db |||||  
917 CTCAGAATCAGGCAAAAGACTTTATTTCGGCACCTTCTGGAGCGAGACCTTCAGAAGAGGTT 976  
QY 881 CACCTGCCAGGCCCCCTACAGCATCTTTGGATCTCTGGGATGCGAGCCTTCGATAGGGA 940  
Db |||||  
977 CACCTGCCAACAGGCCCTTGGGACCTTTGGATCTTTGGGACACAGGCTTTGGCAGGGA 1036  
QY 941 CATCCTGGGTTCTGTCAGTGAGCAGATCCAGAAAGAAATTTTGGCAGGACCCACTGGAAGCG 1000  
Db |||||  
1037 CATCTTAGGGTTGTCAGTGAGCAGATCCGGAAGAACTTTGCTTGGACACACTGGAAGCG 1096  
QY 1001 TGCATTCAATGCCACATCATCTCCTACGTCATCCGTAAGCTGGGACAAAGCCAGAGGG 1060  
Db |||||  
1097 AGCCTTCAATGCCACCTTGTTCCTGCGCCACATCCGGAAGCTGGGGCAGATCCCAGAGGG 1156  
QY 1061 TGAGGAGGCCCTCAGGCAGTGTATGACCCGTATAGCCACCCAGGCCCTTGGGACTAGCCA 1120  
Db |||||  
1157 CGAGGGGGCCTCTGAGCAGGGCATGGSCCGNCACAGCCACTNAGGCCCTTCGTGTGGCCA 1216  
QY 1121 GTCCCCCAAGTGGTGA AAAA C CAGGTAGATGCCAAGGAAGGCCAAGTGGAGTCACTCCCGG 1180  
Db |||||  
1217 GCCCCCCAAGTGGTATGCCCAGGNAGATGCC----GAGGCCAAGTGGGANTGANCCCCAG 1272  
QY 1181 TTTTCTTTC 1190  
Db |||||  
1273 ATTNCTTNC 1282

RESULT 7







QY	627	ACCC	CAGG	ATAT	GTGG	CCCC	CAGAG	CTCT	GGAG	CAGAA	CCCT	ACGG	AAGG	CCG	TAGAT	686	
Db	242	ACCC	CTGG	ATAT	GTGG	CCCC	CAGAG	CTCT	GGAG	CAGAA	CCCT	ACGG	AAGG	CCG	TAGAT	301	
QY	687	GTGT	GGGC	CCCT	GGGT	GTG	TCAT	CTCT	CATAC	ATCCT	GTGT	GGGT	ATAC	CCCC	CCCT	TTCTATGAT	746
Db	302	GTGT	GGGC	CCCT	GGGC	GTG	TCAT	CTCT	CATAC	ATCCT	GTGT	GGGT	ATAC	CCCC	CCCT	TTCTACGAC	361
QY	747	GAGAG	CGGAT	CCCT	GAACT	CTTTC	AGCC	CAGATT	CTG	AGGG	CCAGCT	ATG	AGTT	TGACT	TC	CCCC	806
Db	362	GAGAG	CGAC	CCCT	GAGCT	CTTTC	AGCC	CAGAT	CTG	AGGG	CCAGCT	ATG	AGTT	TGACT	TC	CCT	421
QY	807	TTTT	GGGAT	GACAT	CTC	AGAA	TCAG	CCAA	AGACT	TTCA	TTCC	GCAC	CTTCT	TG	GAAC	GTGAT	866
Db	422	TTCT	GGGAT	GACAT	CTC	AGAA	TCAG	CCAA	AGACT	TTCA	TTCC	GCAC	CTTCT	TG	GAAC	GTGAGAC	481
QY	867	CCCC	AGAAG	AGGTT	CACT	CTGCC	AGCG	CCCT	TAC	AGCAT	CTTT	TGAT	CTCT	TGGG	GATGCA	926	
Db	482	CCCC	AGAAG	AGGTT	CACT	CTGCC	AAAC	AGGCC	CTT	GCGG	CACT	TTT	TGAT	CTCT	TGGG	GACACA	541
QY	927	GCCT	TCGAT	AGG	GACAT	CTCT	GGGT	TTCT	GT	CAGT	GAGC	AGAT	CC	AGA	AATTT	TGCCAGG	986
Db	542	GCCT	TCGA	CAGG	GACAT	CTT	AGG	CTCT	GT	CAGT	GAGC	AGAT	CC	AGA	AATTT	TGCTCGG	601
QY	987	ACCC	ACTG	GAAG	CGT	GCATT	CAAT	TGCC	ACAT	CAT	TTCT	CCTAC				1026	
Db	602	ACAC	ACTG	GAAG	CGAG	CGCT	TTCA	ATG	CCAC	CTCG	TTCT	CTG	C			641	

## RESULT 10

US-10-204-041-9  
; Sequence 9, Application US/10204041  
; Publication No. US20030176443A1

: GENERAL INFORMATION:

APPLICANT: STEIN-GERLACH, MATTHIAS  
APPLICANT: SALASSIDIS, KONSTADINOS

APPLICANT: BACHER, GERALD

: APPLICANT: MÜLLER, STEFFAN

APPLICANT:	MOLLER, STEFAN
TITLE OF INVENTION:	Pyridylpyrimidine Derivatives as Effective Compounds Against Prio
TITLE OF INVENTION:	Infections and Prio Diseases

; FILE REFERENCE: AXM-007.1P US

REFERENCE: FRM 007.1F 00  
; CURRENT APPLICATION NUMBER: US/10/204,041

CURRENT REFLECTION NUMBER: 03/1  
CURRENT FILING DATE: 2002-08-16

: PRIOR APPLICATION NUMBER: EP 011117858.5  
 : CURRENT FILING DATE: 2002-08-18

; PRIOR APPLICATION NUMBER: 2001-05-16  
: PRIOR FILING DATE: 2001-05-16

;  
; PRIOR FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: PCT/EP02/05420

;; PRIOR APPLICATION NUMBER: PCI  
: PRIOR FILING DATE: 2002-05-16

; PRIOR FILING DATE: 2002-11-01  
 ; NUMBER OF SEQ ID NOS: 20

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; NUMBER OF SEQ ID NOS: 20
: SOFTWARE: Patent version 3.1

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; SOFTWARE: 1  
: CEO ID NO 9

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; SEQ ID NO 9
: LENGTH: 1480

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LENGTH: 1.  
TYPE: DNA

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; TYPE: DNA
; ORGANISM: Homo sapiens

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ORGANISM  
FEATURE:

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; FEATURE:
: NAME/KEY: misc feature
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; NAME/KEY: MISC_FEATURE
; LOCATION: (104) (106)

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; LOCATION: (I04) :: (I06)
; OTHER INFORMATION: n = a. c. a or t

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**OTHER INFO:**

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; FEATURE:
: NAME/KEY: misc feature

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; NAME/KEY: "TSC"
; LOCATION: (118)..(118)

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LOCATION: (118) : (118)  
OTHER INFORMATION: n = a, c, q or t

US-10-204-041-9

Query Match	32.2%	Score 500.8;	DB 16;	Length 1480;
Best Local Similarity	72.0%	Pred. No. 1.8e-144;		
Matches 668;	Conservative	0;	Mismatches 257;	Indels 3; Gaps 1;

Qy	119	GAACAGACGGAGGACATCAGCAGTGCTATGATCCGGAGAGAGCTGGGCTCGGGTGC	178
Db	177	GAAGCAGCGGAGGACATTAGAGACATCTACGACTCCGAGATGTTCTGGGCACGGGGC	236
Qy	179	CTTCTCTGAGGTGATGCTGCCCCAGGAAGGGGCTCTGCTCATCTTGTGGCCCTCAAGTG	238

## RESULT 11

RES001 II  
US-10-305-720-1454

US-10-303-720-1454  
: Sequence 1454, Application US/10305720; sequence 1434, Application US/1  
; Publication No. US20040010136A1; PUBLICATION NO: US20  
: GENERAL INFORMATION:

APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.

: TITLE OF INVENTION: Composition for the D

FILE OF INVENTION: COMPOSITE  
FILE REFERENCE: PA-0002-1 CON

FILE REFERENCE: RA 0002 1 COM  
: CURRENT APPLICATION NUMBER: US/10/305,720

: CURRENT FILING DATE: 2002-11-26  
: CURRENT APPLICATION NUMBER: 00/11-26

; CURRENT FILING DATE: 2002-11-29  
 ; PRIOR APPLICATION NUMBER: 09/016,434

; PRIOR FILING DATE: 1998-01-30

; FROM FILING DATE: 1998-01-01  
; NUMBER OF SEQ ID NOS: 1490

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; NUMBER OF DEY IS NOO:
; SOFTWARE: PERL Program

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QY 539 CACACCTTTTGAGGACTCCAAAGATCATGGTCTCTGACTTTGGCCTGTGCCAAATACAAAG- 597  
Db 628 CAGCCTGGATGAAGACTCCAAAATCATGATCTCCGACTTTGGCCTCTCCAAGATGGAGGA 687  
QY 598 --CTGGCAACATGCTAGGCACAGCCTGTGGGACCCAGGATATGTGGCCCTCAGAGCTCCT 655  
Db 688 CCGGGCAGTGTGCTCTCCACCGCCTGTGGAACCTCCGGGATACGTGGCCCTGAAGTCT 747  
QY 656 GGAGCAGAAACCCCTACGGGAAGCCGTAGATGTGTGGCCCTGGGTGTCTATCTCTACAT 715  
Db 748 GGCCAGAGCCCTACAGCAAGGCTGTGGATTGCTGTCTCATAGGTGTCTATCGCTACAT 807  
QY 716 CCTGCTGTGGGTACCCCCCTTCTATGATGAGAGCGGATCCTGAACTCTTTCAGCCAGAT 775  
Db 808 CTGCTCTGGGTTACCTCTCCCTTCTATGACGAGATGATGCCAAACTCTTTGAAACAGAT 867  
QY 776 TCTGAGGGCCAGCTATGAGTTTGTACTCCCTTTTGGGATGACATCTCAGAAATCAGCCAA 835  
Db 868 TTTGAAGGCCGAGTACGAGTTTGTACTCTCTTACTGGGACGACATCTCTGACTCTGCCAA 927  
QY 836 AGACTTCATTTCGCCACCTTCTTGGAAAGTGTATCCCAAGAGAGTTTCACTGCCAGCAGGC 895  
Db 928 AGATTTCATCCGGCATTGTATGGAGAGGACCCAGAGAAAGATTACCTGTGAGCAGGC 987  
QY 896 CCTACAGCATCTTTGGATCTCTGGGATGCAGCCCTTCGATAGGGACATCCTGGGTTCTGT 955  
Db 988 CTTGCAGCACCCTATGGATTGCAGGAGATACAGCTTAGATAAGAAATATCCACCAGTGGT 1047  
QY 956 CAGTGAGCAGATCCAGAAAGAAATTTGCCAGGACCCACTGGAAGCGTGATTCATTCGCCAC 1015  
Db 1048 GAGTGAGCAGATCAAGAAAGAACTTTGCCAAGAGCAAGTGGAAAGCAAGCCTTCAATGCCAC 1107  
QY 1016 ATCATTCCTACGTACATCCGTAAGCTG 1043  
Db 1108 GGCTGTGGTGCAGCACATGAGGAAACTG 1135

RESULT 13

US-09-733-388-3  
; Sequence 3, Application US/09733388  
; Publication No. US20030064495A1  
; GENERAL INFORMATION:  
; APPLICANT: Donoho, Greg  
; APPLICANT: Scoville, John  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Abuin, Alejandro  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: No. 6602698el Human Kinase Proteins and  
; TITLE OF INVENTION: Polynucleotides Encoding the Same  
; FILE REFERENCE: LEX-0103-USA  
; CURRENT APPLICATION NUMBER: US/09/733,388  
; CURRENT FILING DATE: 2000-12-07  
; PRIOR APPLICATION NUMBER: US 60/169,428  
; PRIOR FILING DATE: 1999-12-07  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 1074  
; TYPE: DNA  
; ORGANISM: Homo sapiens

US-09-733-388-3

Query Match 28.1%; Score 436.2; DB 10; Length 1074;  
Best Local Similarity 67.6%; Pred. No. 1.9e-124;  
Matches 628; Conservative 0; Mismatches 298; Indels 3; Gaps 1;  
QY 117 AAGAAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAGCTGGGCTCGGGT 176  
Db 37 AAAAGCAAGCTGAAGACATCAAGAAGATCTTCGAGTTCAAAGAGACCCCTCGGAACCGGG 96

QY 177 GCCTTCTCTGAGGTGATGCTGGCCCAAGAAAGGGGCTCTGCTCATCTTGTGGCCCTCAAG 236  
Db 97 GCCTTTTCCGAAGTGGTTTTAGCTGAAGAGAAAGGCAACTGGCAAGCTCTTTGCTGTGAAG 156  
QY 237 TGCATTCCCAAGAAAGCACTTCGGGGCAAGGAGGCGCCTGGTGGAGAAATGAGATCGCGTA 296  
Db 157 TGTATCCCTAAGAAAGGCGCTGAAGGGCAAGGAACGACATAGAGAAATGAGATAGCCGTC 216  
QY 297 CTTCCGAGAATCAGCCATCCCAACATTGTGGCTCTGGAGGACGTCATGAGATCCTTCT 356  
Db 217 CTGAGAAAGATTAAAGCATGAAAATAATTGTTGCCCTGGAAGACATTTATGAAAGCCCAAT 276  
QY 357 CATCTCTACTTGGCCATGGAGCTGGTAACAGAGTGTGAACCTTTTGACCGCATCATGGAG 416  
Db 277 CACCTGTACTTGGTTCATGTCAGCTGGTGTCCGGTGGAGAGCTGTTTGACCGGATAGTGGAG 336  
QY 417 CGGGGCTCTACACAGAGAAAGGACGCCAGCCACCTTGTAGGGCAGGTCCTTGGCGCTGTC 476  
Db 337 AAGGGGTTTTATACAGAGAAAGGATGCCAGCCTCTGATCCGCCAAGTCTTGGACGCCGTG 396  
QY 477 TCCTACCTTCATAGCCTGGGCATCGTGCAACGGGACCTCAAGCCTGAAAAACCTCTCTAT 536  
Db 397 TACTATCTCCACAGAAATGGGCATCGTCCACAGAGACCTCAAGCCCCGAAAATCTCTGTAC 456  
QY 537 GCCACACCTTTTGAAGACTCCAAGATCATGGTCTCTGACTTTGGCCTGTCCAAAAATACAA 596  
Db 457 TACAGTCAAGATGAGGAGTCCAAAATAATGATCAGTGAATTTGGATTGTCAAAAATGGAG 516  
QY 597 G---CTGGCAACATGCTAGGCACAGCCTGTGGGACCCAGGATATGTGGCCCAAGAGCTC 653  
Db 517 GGCAAGGAGATGTGATGTCCACTGCCCTGTGGAACTCCAGGCTATGTGCTCCTGAAGTC 576  
QY 654 CTGGAGCAGAAACCCCTACGGGAAGGCCGTAGATGTGGGCCCTGGGTGTCTATCTCTAC 713  
Db 577 CTCGCCCAGAAACCTTACAGCAAGCCGTTGACTGTGTGTCATCGGAGTGAATGCTGTAC 636  
QY 714 ATCTGTGTGGGTACCCCTTCTATGATGAGAGCGGATCCTGAACTCTTCAGCCAG 773  
Db 637 ATCTTGCTCTGGGCTACCTCTCTTTTATGATGAAAATGACTCCAAGCTCTTTGAGCAG 696  
QY 774 ATTCTGAGGGCCAGCTATGAGTTTGAATCTCCCTTTTGGGATGACATCTCAGAAATCAGCC 833  
Db 697 ATCTCAAGGGGGAATATGAGTTTGAATCTCTCTTACTGGGATGACATCTCCGACTCTGCA 756  
QY 834 AAAGACTTCATTGCCACCTTCTGGAACTGTATCCCAAGAGAGTTTCACTGCCAGCAG 893  
Db 757 AAAGACTTCATTCCGAACTGTATGGAGAGGACCCGAAATAAAGATACACGCTGTGAGCAG 816  
QY 894 GCCCTACAGCATCTTTGGATCTCTGGGGATGCGAGCCTTCGATAGGGACATCTCTGGTCT 953  
Db 817 GCAGCTCGGCACCCATGGATGCTGTGTGACACAGCCCTCAACAAAAACATCCACGAGTCC 876  
QY 954 GTCAGTGAGCAGATCCAGAAAGAAATTTTGGCAGGACCCACTGGAAGCGTGCATTCATGCC 1013  
Db 877 GTCAGCGCCAGATCCGGAATACTTTGCCAAGAGCAAAATGGAGACAAGCATTTAATGCC 936  
QY 1014 ACATCATTCCTACGTACATCCGTAAGCT 1042  
Db 937 ACGGCCGTCGTGAGACATATGAGAAAACT 965

RESULT 14

US-10-024-036B-3  
; Sequence 3, Application US/10024036B  
; Publication No. US20030028004A1  
; GENERAL INFORMATION:  
; APPLICANT: Bandaru, Rajasekhar  
; TITLE OF INVENTION: 68730 and 69112, Protein Kinase  
; TITLE OF INVENTION: Molecules and Uses Therefor  
; FILE REFERENCE: MPI2000-521P1R(M)  
; CURRENT APPLICATION NUMBER: US/10/024,036B  
; CURRENT FILING DATE: 2001-12-17  
; PRIOR APPLICATION NUMBER: 60/258222



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; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1074
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-024-036B-3

Query Match      28.1%; Score 436.2; DB 14; Length 1074;
Best Local Similarity 67.6%; Pred. No. 1.9e-124;
Matches 628; Conservative 0; Mismatches 298; Indels 3; Gaps 1;

QY 117 AAGAAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAAAGCTGGGCTCGGGT 176
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 37 AAAAAGCAAGCTGAAGACATCAAGAAGATCTTCGAGTTCAAAGAGACCCCTCGGAACCGGG 96

QY 177 GCCTTCTCTGAGGTGATGCTGGCCAGGAAAGGGCTCTGCTCATCTTGTGGCCCTCAAG 236
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 97 GCCTTTTCCGAAGTGGTTTTAGCTGAAGAGAAAGGCAAACTGGCAAGCTCTTGTGTGAAG 156

QY 237 TGCATTTCCCAAGAAACACTTCGGGGCAAGAGGCCCTGGTGGAGAAATGAGATCGCGGTA 296
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 157 TGTATCCCTAAGAAAGCGCTGAAGGGCAAGGAAAGCAGCATAGAGAATGAGATAGCCGTC 216

QY 297 CTTCGCAGAATCAGCCATCCCAACATTTGGCTCTGGAGGACGTCCATGAGAGTCTTCT 356
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 217 CTGAGAAAGATTAAAGCATGAAAATATTGTTGCCCTGGAAGACATTTATGAAAGCCCAAT 276

QY 357 CATCTCTACTTGGCCATGGAGTGGTAAACAGGTGGTGAACCTGTTGACCGCATCATGGAG 416
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 277 CACCTGTACTTGGTCATGCAGCTGGTGTCCGGTGGAGAGCTGTTGACCCGATAGTGGAG 336

QY 417 CGGGGCTCTACACAGAGAAAGGACGCCACCTTGTAGGGCAGGTCTTGTAGGCGGTGTC 476
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 337 AAGGGGTTTTATACAGAGAAAGGATGCCAGCACTCTGCTCATCTTGTGGCCCTCAAG 216

QY 297 CTTCGCAGAATCAGCCATCCCAACATTTGGCTCTGGAGGACGTCCATGAGAGTCTTCT 356
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 217 CTGAGAAAGATTAAAGCATGAAAATATTGTTGCCCTGGAAGACATTTATGAAAGCCCAAT 276

QY 357 CATCTCTACTTGGCCATGGAGTGGTAAACAGGTGGTGAACCTGTTGACCGCATCATGGAG 416
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 277 CACCTGTACTTGGTCATGCAGCTGGTGTCCGGTGGAGAGCTGTTGACCCGATAGTGGAG 336

QY 417 CGGGGCTCTACACAGAGAAAGGACGCCACCTTGTAGGGCAGGTCTTGTAGGCGGTGTC 476
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 337 AAGGGGTTTTATACAGAGAAAGGATGCCAGCACTCTGCTCATCTTGTGGCCCTCAAG 216

QY 297 CTTCGCAGAATCAGCCATCCCAACATTTGGCTCTGGAGGACGTCCATGAGAGTCTTCT 356
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 217 CTGAGAAAGATTAAAGCATGAAAATATTGTTGCCCTGGAAGACATTTATGAAAGCCCAAT 276

QY 357 CATCTCTACTTGGCCATGGAGTGGTAAACAGGTGGTGAACCTGTTGACCGCATCATGGAG 416
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 277 CACCTGTACTTGGTCATGCAGCTGGTGTCCGGTGGAGAGCTGTTGACCCGATAGTGGAG 336

QY 417 CGGGGCTCTACACAGAGAAAGGACGCCACCTTGTAGGGCAGGTCTTGTAGGCGGTGTC 476
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Db 337 AAGGGGTTTTATACAGAGAAAGGATGCCAGCACTCTGCTCATCTTGTGGCCCTCAAG 216

QY 477 TCCTACCTTCATAGCCTGGGCATCGTGCAACCGGACCTCAAGCCTGAAACCTCCTCTAT 536
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Db 397 TACTATCTCCACAGAAATGGGCATCGTCCACAGAGAGACCTCAAGCCCGAAATCTCTTGTA 456

QY 537 GCCACACCTTTTGGAGTCCCAAGATCATGGTCTGTAACAGGTGGTGAACCTGTTGACCGCATCATGGAG 596
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QY 597 G---CTGGCAACATGTAGGCACAGCCTGTGGGACCCCGAGGATATCTGGCCCTGTCAAAATACAA 653
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QY 654 CTGGAGCAGAAACCTACGGGAAGGCCGTAGATGTGTGGGCCCTTGGGTGTCTCTCTAC 713
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Db 577 CTCGCCCAGAAACCTTACAGCAAAAGCCGTTGACTGCTGGTCCATCGGAGTGAATGCCTAC 636

QY 714 ATCCTGCTGTGTGGGTACCCCTTCTATATGATGAGAGCGATCCTGAACCTTTCAGCCAG 773
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Db 697 ATCCTCAAGCGGGAATATGAGTTTGAATCTCCCTACTGGGATGACATCTCCGACTCTGCA 756

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Db 757 AAAGACTTCATTCCGGAACCTGATGGAGAGGACCCCAATAAAGATACACGTTGTGAGCAG 816

QY 894 GCCCTACAGCATCTTTGGATCTCTGGGGATGCAGCCTTCGATAGGGACATCTTGGGTTCT 953
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Db 817 GCAGCTCGGCACCCCATGGATCGCTGGTGACACAGAGCCCTCAACAAAAACATCCACGAGTCC 876

QY 954 GTCAGTGAGCAGATCCAGAGAAATTTTGGCAGGACCCACTGGAGCGTGCATTCATGCCC 1013
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RESULT 15
US-10-446-175-3
; Sequence 3, Application US/10446175
; Publication No. US20040014112A1
; GENERAL INFORMATION:
; APPLICANT: Donoho, Greg
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Abuin, Alejandro
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: No. US20040014112A1el Human Kinase Proteins and
; FILE REFERENCE: Polynucleotides Encoding the Same
; CURRENT APPLICATION NUMBER: US/10/446,175
; CURRENT FILING DATE: 2003-05-27
; PRIOR APPLICATION NUMBER: US/09/733,388
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,428
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1074
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-446-175-3

Query Match      28.1%; Score 436.2; DB 17; Length 1074;
Best Local Similarity 67.6%; Pred. No. 1.9e-124;
Matches 628; Conservative 0; Mismatches 298; Indels 3; Gaps 1;

QY 117 AAGAAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAAAGCTGGGCTCGGGT 176
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Db 37 AAAAAGCAAGCTGAAGACATCAAGAAGATCTTCGAGTTCAAAGAGACCCCTCGGAACCGGG 96

QY 177 GCCTTCTCTGAGGTGATGCTGGCCAGGAAAGGGCTCTGCTCATCTTGTGGCCCTCAAG 236
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Db 97 GCCTTTTCCGAAGTGGTTTTAGCTGAAGAGAAAGGCAAGGACGATAGAGAATGAGATAGCCGTC 216

QY 237 TGCATTTCCCAAGAAACACTTCGGGGCAAGAGGCCCTGGTGGAGAAATGAGATCGCGGTA 296
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db 337 AAGGGGTTTTATACAGAGAAAGGATGCCAGCACTCTGCTCATCTTGTGGCCCTCAAG 216

QY 477 TCCTACCTTCATAGCCTGGGCATCGTGCAACCGGACCTCAAGCCTGAAACCTCCTCTAT 536
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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QY 537 GCCACACCTTTTGGAGTCCCAAGATCATGGTCTGTAACAGGTGGTGAACCTGTTGACCGCATCATGGAG 596
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Db 517 GGCAAAAGGAGATGTGATGTCCACTGCCTGTGGAACCTCAGGCTATGTGCTCTGTAAGTC 576

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Db 577 CTCGCCCAGAAACCTTACAGCAAAAGCCGTTGACTGCTGGTCCATCGGAGTGAATGCCTAC 636

QY 714 ATCCTGCTGTGTGGGTACCCCTTCTATATGATGAGAGCGATCCTGAACCTTTCAGCCAG 773
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Db 637 ATCTTGCTCTGCGGCTACCCCTCCTTTTATGATGAAATGACTCCAAGCTCTTTGAGCAG 696

QY 774 ATTCTGAGGGCCAGCTATGAGTTTGAATCCCTTTTGGGATGACATCTCAGAATCAGCC 833
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Db 697 ATCCTCAAGCGGGAATATGAGTTTGAATCTCCCTACTGGGATGACATCTCCGACTCTGCA 756

QY 834 AAAGACTTCATTCCGCCACCTTCTGGAACGTGATCCCAAGAGAGGTTTCACTGCGCAGCAG 893
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Db 757 AAAGACTTCATTCCGGAACCTGATGGAGAGGACCCCAATAAAGATACACGTTGTGAGCAG 816

QY 894 GCCCTACAGCATCTTTGGATCTCTGGGGATGCAGCCTTCGATAGGGACATCTTGGGTTCT 953
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 817 GCAGCTCGGCACCCCATGGATCGCTGGTGACACAGAGCCCTCAACAAAAACATCCACGAGTCC 876

QY 954 GTCAGTGAGCAGATCCAGAGAAATTTTGGCAGGACCCACTGGAGCGTGCATTCATGCCC 1013
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 877 GTCAGCGCCAGATCCCGGAAAAACTTTTGCCAAGAGCAAAATGGAGACAAGCAATTTAATGCC 936
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QY	654	CTGGAGCAGAAACCCCTACGGGAAGCCGCTAGATGTGTGGGCCCTGGGTGTCACTCCTAC	713
Db	577	CTCGCCCAGAAACCTTACAGCAAAAGCCGTTGACTGCTGGTCCATCGGAGTGATTGCCTAC	636
QY	714	ATCCTGCTGTGTGGGTACCCCCCTTCTATGATGAGAGCGATCCTGAACTCTTCAGCCAG	773
Db	637	ATCTTGCTCTGCGGCTACCCCTCTTTTATGATGAAAATGACTCCAAGCTCTTTGAGCAG	696
QY	774	ATTCTGAGGCCAGCTATGAGTTTGACTCCCCCTTTTGGGATGACATCTCAGAATCAGCC	833
Db	697	ATCCTCAAGCGGGAATATGAGTTTGACTCTCCCTACTGGGATGACATCTCCGACTCTGCA	756
QY	834	AAAGACTTCATTCCGCCACCTTCTTGGAACTGTATCCCCAGAAAGAGTTTCACTGCCAGCAG	893
Db	757	AAAGACTTCATTCCGGAACCTGATGGAGAGGACCCCGAATAAAGATACACCGTGTGAGCAG	816
QY	894	GCCCTACAGCATCTTTGGATCTCTGGGGATGCAGCCTTCGATAGGGACATCCTGGGTCT	953
Db	817	GCAGCTCGGCACCCCATGGATCGCTGGTGACACAGCCCTCAACAAAAACATCCACGAGTCC	876
QY	954	GTCAGTGAGCAGATCCAGAAGAAATTTGCCAGGACCCACTGGAAGCGTGCAATCAATGCC	1013
Db	877	GTCAGGCCCCAGATCCGGGAAAAACTTTGCCAAGAGCAAAATGGAGACAAGCATTTAATGCC	936
QY	1014	ACATCATTCCTACGTACATCCGTAAGCT	1042
Db	937	ACGGCCGTCGTGAGACATATGAGAAAACT	965

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 6, 2005, 08:23:56 ; Search time 52 Seconds  
(without alignments)  
5750.802 Million cell updates/sec

Title: US-10-032-254A-1  
Perfect score: 2872  
Sequence: 1 gttgcggagtccttcactc.....caaaaaaaaaaaaaaa 1554

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ n2p.model -DEV=xlp  
-Q=/cgn2\_1/USFTO\_spool\_p/US10032254/runat\_02062005\_131019\_3607/app\_query.fasta\_1.1735  
-DB=PIR\_79 -QFMT=fastan -SUFFIX=xpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=Dits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM\_ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10032254 @CGN\_1\_1\_41 @runat\_02062005\_131019\_3607 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : PIR\_79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1188.5	41.4	374	1 S50193	Ca2+/calmodulin-de
2	1184.5	41.2	370	1 S57347	Ca2+/calmodulin-de
3	1010.5	35.2	348	2 T37321	Ca2+/calmodulin-de
4	874.5	30.4	310	2 B88640	protein X07A9.2 [i
5	730	25.4	473	1 A53036	Ca2+/calmodulin-de
6	724.5	25.2	474	1 TVRTC4	Ca2+/calmodulin-de
7	722.5	25.2	502	2 I52637	Ca2+/calmodulin-de
8	719	25.0	469	1 S17656	Ca2+/calmodulin-de
9	717	25.0	504	2 I56542	calmodulin-binding
10	705	24.5	421	2 T30814	calmodulin-binding
11	695	24.2	301	1 A40811	myosin-light-chain
12	647	22.5	414	2 JN0323	Ca2+/calmodulin-de
13	638	22.2	335	2 T50290	calmodulin kinase
14	611.5	21.3	509	2 B44412	calmodulin-depende

15	611.5	21.3	516	1 JU0270	Ca2+/calmodulin-de
16	611.5	21.3	530	2 D44412	Ca2+/calmodulin-de
17	594.5	20.7	478	1 A30355	Ca2+/calmodulin-de
18	593.5	20.7	589	2 S68470	Ca2+/calmodulin-de
19	591.5	20.6	518	1 S43845	Ca2+/calmodulin-de
20	591	20.6	508	1 A43713	calcium-dependent
21	589.5	20.5	478	1 S04365	Ca2+/calmodulin-de
22	589	20.5	527	1 A31908	Ca2+/calmodulin-de
23	588	20.5	490	2 T08873	calcium-dependent
24	587	20.4	610	1 A49082	calcium-dependent
25	586	20.4	520	2 C84774	probable calcium-d
26	586	20.4	531	1 T02993	calcium-dependent
27	584.5	20.4	639	1 T02784	calcium-dependent
28	584	20.3	518	1 B46619	Ca2+/calmodulin-de
29	584	20.3	556	2 JC5636	Ca2+/calmodulin-de
30	582	20.3	446	2 A40896	calcium-dependent
31	582	20.3	513	1 T02259	calcium-dependent
32	581	20.2	504	2 T38226	probable serine-th
33	580.5	20.2	708	2 T23616	hypothetical prote
34	580	20.2	533	1 A34366	Ca2+/calmodulin-de
35	580	20.2	580	2 T40939	probable Ca-calmod
36	578.5	20.1	554	2 T05476	calcium-dependent
37	578	20.1	490	1 S71776	calcium-dependent
38	578	20.1	583	2 H84810	probable calcium-d
39	576	20.1	542	1 A45025	Ca2+/calmodulin-de
40	574	20.0	495	1 S46284	calcium-dependent
41	574	20.0	501	2 G85097	hypothetical prote
42	574	20.0	542	1 A26464	Ca2+/calmodulin-de
43	570.5	19.9	553	1 T02139	calcium-dependent
44	570	19.8	447	2 B40896	Ca2+/calmodulin-de
45	569.5	19.8	531	2 D85059	probable calcium d

ALIGNMENTS

RESULT 1

S50193  
Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) I - rat  
N;Alternate names: CamKI  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: S50193; A49682; A46038  
R;Cho, F.S.; Phillips, K.S.; Bogucki, B.; Weaver, T.E.  
Biochim. Biophys. Acta 1224, 156-160, 1994  
A;Title: Characterization of a rat cDNA clone encoding calcium/calmodulin-dependent pr  
A;Reference number: S50193; MUID:95035115; PMID:7948038  
A;Accession: S50193  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-374 <CHO>  
A;Cross-references: UNIPROT:Q63450; EMBL:L26288; NID:g439613; PIDN:AAA66944.1; PID:g439  
R;Picciotto, M.R.; Czernik, A.J.; Nairn, A.C.  
J. Biol. Chem. 268, 26512-26521, 1993  
A;Title: Calcium/calmodulin-dependent protein kinase I. cDNA cloning and identification  
A;Reference number: A49682; MUID:94075341; PMID:8253780  
A;Accession: A49682  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-111,'G',113-117,'R',119-308,'R',310-322,'HQPG',327,'T',329,'TDS' <PIC>  
A;Cross-references: GB:L24907; NID:g406112; PIDN:AAA19670.1; PID:g406113  
R;Mochizuki, H.; Ito, T.; Hidaka, H.  
J. Biol. Chem. 268, 9143-9147, 1993  
A;Title: Purification and characterization of Ca2+/calmodulin-dependent protein kinase  
A;Reference number: A46038; MUID:93232082; PMID:8386178  
A;Accession: A46038  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 12-36,'T' <MOC>  
A;Experimental source: cerebrum  
A;Note: sequence extracted from NCBI backbone (NCBIP:129927)  
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C;Keywords: ATP; autophosphorylation; calmodulin binding; phosphoprotein; phosphotransf  
F;18-276/Domain: protein kinase homology <KIN>

F;26-34/Region: protein kinase ATP-binding motif  
F;293-299/Region: autoinhibitory  
F;302-314/Region: calmodulin binding  
F;177/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted

Alignment Scores:  
Pred. No.: 9.33e-45 Length: 374  
Score: 1188.50 Matches: 221  
Percent Similarity: 85.53% Conservative: 51  
Best Local Similarity: 69.50% Mismatches: 43  
Query Match: 41.38% Indels: 3  
DB: 1 Gaps: 2

US-10-032-254A-1 (1-1554) x S50193 (1-374)  
QY 120 AAACAGACGGAGGACATCAGCAGTGTCTATGATCCGGGAGAAAGCTGGGCTCGGTGCC 179  
Db 11 LysGlnAlaGluAspIleArgAspIleTyrAspPheArgAspValLeuGlyThrGlyAla 30  
QY 180 TTCTCTGAGGTGATGCTGGGCCCCAGGAAAGGGGCTCTGCTCATCTTGTGGCCCTCAAGTGC 239  
Db 31 PheSerGluValIleLeuAlaGluAspLysArgThrGlnLysLeuValAlaIleLysCys 50  
QY 240 ATTCCCAAGAAAGCACTTCGGGGCAAGGAGGCCCTGGTGAGAAATGAGATCGCGGTACTT 299  
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QY 300 CGCAGAATCAGCCATCCCAACATTGTGGCTCTGGAGGACGTCCATGAGAGTCTTCTCAT 359  
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QY 360 CTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAAGTGTGGACCGCATCATGGAGCGG 419  
Db 91 LeuTyrLeuIleMetGlnLeuValSerGlyGlyGluLeuPheAspArgIleValGluLys 110  
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QY 480 TACCTTCATAGCCTGGGCATCGTGACCGGACCTCAAGCCTGAAAACCTCCTCTATGCC 539  
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QY 540 ACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTGGCCTGTCCAAATACAA--- 596  
Db 151 SerLeuAspGluAspSerLysIleMetIleSerAspPheGlyLeuSerLysMetGluAsp 170  
QY 597 GCTGGCAACATGCTAGGCACAGCCTGTGGGACCCACGATATGTGGCCCCAGAGCTCCTG 656  
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QY 657 GAGCAGAAACCCCTACGGGAAGCCGCTAGATGTGTGGCCCTGGGTGTCTCTCTACATC 716  
Db 191 AlaGlnLysProTyrSerLysAlaValAspCysTrpSerIleGlyValIleAlaTyrIle 210  
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QY 777 CTGAGGGCCAGCTATGAGTTTGACTCCCCCTTTTGGGATGACATCTCAGAATCAGCCAAA 836  
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QY 837 GACTTCATTCCGCCACCTTCTGGAACGTGATCCCCAGAGAGGTTTCAACCTGCCAGCAGGCC 896  
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QY 897 CTACAGCATCTTTGGATCTCTGGGGATGCAGCCTTCGATAGGGACATCCTGGGTCTGTGC 956  
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Db 291 SerGluGlnIleLysLysAsnPheAlaLysSerLysTrpLysGlnAlaPheAsnAlaThr 310  
QY 1017 TCATTCCCTACGTACATCCGTAAG-----CTGGGACAAAGCCAGAGGGTGAG 1064  
Db 311 AlaValValArgHisMetArgLysLeuGlnLeuGlyThrSerGlnGluGlyGln 328  
RESULT 2  
S57347  
Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) I - human  
N;Alternate names: CaMKI  
C;Species: Homo sapiens (man)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: S57347  
R;Haribabu, B.; Hook, S.S.; Selbert, M.A.; Goldstein, E.G.; Tomhave, E.D.; Edelman, A.M.  
EMBO J. 14, 3679-3686, 1995  
A;Title: Human calcium-calmodulin dependent protein kinase I: cDNA cloning, domain structure.  
A;Reference number: S57347; MUID:95369239; PMID:7641687  
A;Accession: S57347  
A;Status: preliminary; nucleic acid sequence not shown  
A;Molecule type: mRNA  
A;Residues: 1-370 <HAR>  
A;Cross-references: UNIPROT:Q14012; EMBL:L41816; NID:g790789; PIDN:AAA99458.1; PID:g790790  
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A;Gene: GDB:CAMK1  
A;Cross-references: GDB:642249  
A;Superfamily: Ca2+/calmodulin-dependent protein kinase I; protein kinase homology  
C;Keywords: ATP; autophosphorylation; calmodulin binding; phosphoprotein; phosphotransf  
F;18-276/Domain: protein kinase homology <KIN>  
F;26-34/Region: protein kinase ATP-binding motif  
F;293-299/Region: autoinhibitory  
F;302-314/Region: calmodulin binding  
F;177/Binding site: phosphate (Thr) (covalent) (by autophosphorylation) #status predicted

Alignment Scores:  
Pred. No.: 1.39e-44 Length: 370  
Score: 1184.50 Matches: 220  
Percent Similarity: 85.53% Conservative: 52  
Best Local Similarity: 69.18% Mismatches: 43  
Query Match: 41.24% Indels: 3  
DB: 1 Gaps: 2  
US-10-032-254A-1 (1-1554) x S57347 (1-370)  
QY 120 AAACAGACGGAGGACATCAGCAGTGTCTATGATCCGGGAGAAAGCTGGGCTCGGTGCC 179  
Db 11 LysGlnAlaGluAspIleArgAspIleTyrAspPheArgAspValLeuGlyThrGlyAla 30  
QY 180 TTCTCTGAGGTGATGCTGGGCCCCAGGAAAGGGGCTCTGCTCATCTTGTGGCCCTCAAGTGC 239  
Db 31 PheSerGluValIleLeuAlaGluAspLysArgThrGlnLysLeuValAlaIleLysCys 50  
QY 240 ATTCCCAAGAAAGCACTTCGGGGCAAGGAGGCCCTGGTGAGAAATGAGATCGCGGTACTT 299  
Db 51 IleAlaLysGluAlaLeuGluGlyLysGluGlySerMetGluAsnGluIleAlaValLeu 70  
QY 300 CGCAGAATCAGCCATCCCAACATTGTGGCTCTGGAGGACGTCCATGAGAGTCTTCTCAT 359  
Db 71 HisLysIleLysHisProAsnIleValAlaLeuAspAspIleTyrGluSerGlyGlyHis 90  
QY 360 CTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAAGTGTGGACCGCATCATGGAGCGG 419  
Db 91 LeuTyrLeuIleMetGlnLeuValSerGlyGlyGluLeuPheAspArgIleValGluLys 110  
QY 420 GGCTCTACACAGAGAAAGGACGCCAGCCACCTTGTAGGGCAGGTCTTGGCGTGTCTCC 479  
Db 111 GlyPheTyrThrGluArgAspAlaSerArgLeuIlePheGlnValLeuAspAlaValLys 130  
QY 480 TACCTTCATAGCCTGGGCATCGTGACCGGACCTCAAGCCTGAAAACCTCCTCTATGCC 539  
Db 131 TyrLeuHisAspLeuGlyIleValHisArgAspLeuLysProGluAsnLeuLeuTyrTyr 150  
QY 540 ACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTGGCCTGTCCAAATACAA--- 596





A;Accession: B88640  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-310 <STO>  
A;Cross-references: GB:chr\_IV; PIDN:AAC68810.1; PID:g3790765; GSPDB:GN00022; CESP:K07A9.  
C;Genetics:  
A;Gene: K07A9.2  
A;Map position: 4  
C;Superfamily: Ca2+/calmodulin-dependent protein kinase I; protein kinase homology

Alignment Scores:  
Pred. No.: 3.8e-31 Length: 310  
Score: 874.50 Matches: 163  
Percent Similarity: 71.96% Conservative: 50  
Best Local Similarity: 55.07% Mismatches: 74  
Query Match: 30.45% Indels: 9  
DB: 2 Gaps: 2

US-10-032-254A-1 (1-1554) x B88640 (1-310)

QY 243 CCCAAGAAAGCACTT-----CGGGGCAAGGAGGCCCTGGTGGAGAATGAG 287  
|||:|||||  
Db 8 ProArgLysLeuLeuTyrProLeuPheAsnLeuSerLysProCysValThrIleAsnGlu 27  
|||:|||||

QY 288 ATCGCGGTA-----CTTCGCAGAAATCAGCCATCCCAACATFTGGCTCTGGAG 335  
|||:|||||  
Db 28 PheLysLeuGluLysPheGluIlePheArgLeuArgHisAsnAsnIleValGlnLeuPhe 47  
|||:|||||

QY 336 GACGTCCATGAGAGTCCTTCTCATCTCTACTTGGCCATGGAGCTGTTAAACAGTGGTGAA 395  
|||:|||||  
Db 48 AspThrTyrAspGluLysGlnPheValTyrLeuValMetGluLeuValThrGlyGlyGlu 67  
|||:|||||

QY 396 CTGTTTGACCGCATCATGGAGCGGGCTCCTACACAGAGAAGGACGCCACCTTGTA 455  
|||:|||||  
Db 68 LeuPheAspArgIleValAlaLysGlySerTyrThrGluGlnAspAlaSerAsnLeuIle 87  
|||:|||||

QY 456 GGGCAGGTCCTTGGCGTGTCTCTCTACCTTATAGCCTGGGCATCGTGCACCGGGACCTC 515  
|||:|||||  
Db 88 ArgGlnValLeuGluAlaValGlyPheMetHisAspAsnGlyValValHisArgAspLeu 107  
|||:|||||

QY 516 AAGCCTGAAAACCTCTCTATGCCACACCTTTTGAGGACTCCAAGATCATGGTCTCTGAC 575  
|||:|||||  
Db 108 LysProGluAsnLeuLeuTyrTyrAsnGlnAspGluAspSerLysIleMetIleSerAsp 127  
|||:|||||

QY 576 TTTGGCCTGTCCAAATACAAGCTGGCAACATGCTAGGCACAGCCTGTGGACCCCGAGGA 635  
|||:|||||  
Db 128 PheGlyLeuSerLysThrGluAspSerGlyValMetAlaThrAlaCysGlyThrProGly 147  
|||:|||||

QY 636 TATGTGCCCCAGAGTCCTGGAGCAGAAACCCCTACGGGAAGGCCGTAGATGTGTGGCC 695  
|||:|||||  
Db 148 TyrValAlaProGluValLeuGlnLysProTyrGlyLysAlaValaspValTrpSer 167  
|||:|||||

QY 696 CTGGGTGTCACTCTCTACATCCTCTGTGTGGGTACCCCCCTTCTATGATGAGAGCGAT 755  
|||:|||||  
Db 168 IleGlyValIleAlaTyrIleLeuLeuCysGlyTyrProProPheTyrAspGluSerAsp 187  
|||:|||||

QY 756 CCTGAACCTTTCAGCCAGATTCTGAGGGCCAGCTATGAGTTTGACTCCCCCTTTTGGGAT 815  
|||:|||||  
Db 188 AlaAsnLeuPheAlaGlnIleIleLysGlyGluTyrGluPheAspAlaProTyrTrpAsp 207  
|||:|||||

QY 816 GACATCTCAGAATCAGCCAAAGACTTTCATTCGCCACCTTCTGGAACGTGATCCCCAGAA 875  
|||:|||||  
Db 208 GlnIleSerAspSerAlaLysAspPheIleThrHisLeuMetCysCysAspProGluAla 227  
|||:|||||

QY 876 AGGTTACCTGCCAGCGCCCTACAGCATCTTTGGATCTCTGGGGATGCGAGCCTTCGAT 935  
|||:|||||  
Db 228 ArgPheThrCysGlnAspAlaLeuSerHisProTrpIleSerGlyAsnThrAlaTyrThr 247  
|||:|||||

QY 936 AGGGACATCTCTGGTTCTGTTCAGTGAGCAGATCCCAAGAATTTTGGCAGGACCCACTGG 995  
|||:|||||  
Db 248 HisAspIleHisGlyThrValAlaValHisLeuLysLysSerLeuAlaLysArgAsnTrp 267  
|||:|||||

QY 996 AAGCGTGCATTCAATGCCACATCATCTCTACGTACATCCGTAAGCTGGGACAAAGCCCA 1055  
|||:|||||

Db 268 LysLysAlaTyrAsnAlaAlaAlaIleArgGlnLeuGlnMetLeuArgIleuSerSer 287  
|||:|||||  
QY 1056 GAGGGTGAGAGGCCTCCAGGCAGTGATGACCCCGTCATAGCCACCCA 1103  
|||:|||||  
Db 288 AsnSerAsnArgLeuGlnLysGlnAlaSerGlnGlnProGluPro 303  
|||:|||||

RESULT 5  
A53036  
N;Alternate names: Ca2+/calmodulin-dependent protein kinase Gr; Cam-kinase IV  
C;Species: Homo sapiens (man)  
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: A53036; JC2261; I53768  
R;MosiAlas, G.; Hanissian, S.H.; Jawahar, S.; Vara, L.; Kieff, E.; Chatila, T.A.  
J. Virol. 68, 1697-1705, 1994  
A;Title: A Ca (2+)/calmodulin-dependent protein kinase, CaM kinase-Gr, expressed after t  
A;Reference number: A53036; MUID:94149862; PMID:8107230  
A;Accession: A53036  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-473 <MSO>  
A;Cross-references: UNIPROT:Q16566; GB:L24959; NID:g407005; PIDN:AAA18251.1; PID:g40700  
R;Kitani, T.; Okuno, S.; Fujisawa, H.  
J. Biochem. 115, 637-640, 1994  
A;Title: cDNA cloning and expression of human calmodulin-dependent protein kinase IV.  
A;Reference number: JC2261; MUID:94375404; PMID:8089075  
A;Accession: JC2261  
A;Molecule type: mRNA  
A;Residues: 1-473 <KIT>  
A;Cross-references: GB:D30742; NID:g487908; PIDN:BAA06403.1; PID:g871845  
R;Bland, M.M.; Monroe, R.S.; Ohmstede, C.  
Gene 142, 191-197, 1994  
A;Title: The cDNA sequence and characterization of the Ca2+/calmodulin-dependent protei  
A;Reference number: I53768; MUID:94252566; PMID:8194751  
A;Accession: I53768  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-473 <RES>  
A;Cross-references: GB:L17000; NID:g306478; PIDN:AAA35639.1; PID:g306479  
C;Comment: This protein is a Ca2+-responsive multifunctional protein kinase, which occu  
s system and in the immune system.  
C;Genetics:  
A;Gene: GDB:ILK  
A;Cross-references: GDB:6155815; OMIM:602366  
A;Map position: 11p15.5-11p15.4  
C;Superfamily: Ca2+/calmodulin-dependent protein kinase; protein kinase homology  
C;Keywords: ATP; calcium binding; calmodulin binding; phosphoprotein; phosphotransferas  
F;44-300/Domain: protein kinase homology <KIN>  
F;52-60/Region: protein kinase ATP-binding motif  
F;320-329/Region: calmodulin binding #status predicted  
F;8,12,15/Binding site: phosphate (Ser) (covalent) #status predicted

Alignment Scores:  
Pred. No.: 6.32e-25 Length: 473  
Score: 730.00 Matches: 154  
Percent Similarity: 63.53% Conservative: 62  
Best Local Similarity: 45.29% Mismatches: 110  
Query Match: 25.42% Indels: 14  
DB: 1 Gaps: 5

US-10-032-254A-1 (1-1554) x A53036 (1-473)

QY 87 GCAAGCAGGTCGCAGACATGCTGTGCTCAAGAAACAGACGGAGGACATCAGCAGTGT 146  
|||:|||||  
Db 26 AlaSerLeuValProAspTyrTrpIleAspGlySerAsnArgAspAlaLeuSerAspPhe 45  
|||:|||||

QY 147 TATGAGATCCGGGAGAAGCTGGGCTCGGCTGCTTCTCTGAGGTGATGCTGCCCAGGAA 206  
|||:|||||  
Db 46 PheGluValGluSerGluLeuGlyArgGlyAlaThrSerIleValTyrArgCysLysGln 65  
|||:|||||

QY 207 AGGGGCTCTGCTCATCTTGTGGCCCTCAAGTGCATTTCCCAAGAAAGCACCTTCGGGGCAAG 266  
|||:|||||

Db 66 LysGlyThrGlnLysProTyrAlaLeuLysValLeuLysLysThrVal-----Assp 82

QY 267 GAGGCCCTGGTGGAGAATGAGATCGCGGTACTTCGAGAAATCAGCCATCCCAACATTGTG 326

Db 83 LysLysIleValArgThrGluIleGlyValLeuLeuArgLeuSerHisProAsnIleIle 102

QY 327 GCTCTGGAGGACGTCATGAGAGTCCTTCTCATCTCTACTTGGCCATGGAGCTGGTAACA 386

Db 103 LysLeuLysGluIlePheGluThrProThrGluIleSerLeuValLeuGluLeuValThr 122

QY 387 GGTGGTGAACCTGTTGACCGCATCATGGAGCGGGCTCTTACACAGAGAAAGGACGCCAGC 446

Db 123 GlyGlyGluLeuPheAspArgIleValGluLysGlyTyrTyrSerGluArgAspAlaAla 142

QY 447 CACCTTGTAGGCGAGTCCTTGGCGCTGTCTCCTACCTTCATAGCCCTGGGCATCGTGCAC 506

Db 143 AspAlaValLysGlnIleLeuGluAlaValAlaTyrLeuHisGluAsnGlyIleValHis 162

QY 507 CGGGACCTCAAGCCCTGAACCTCCTCTATGCCACACCTTTTGAGGACTCCAGATCATG 566

Db 163 ArgAspLeuLysProGluAsnLeuLeuTyrAlaThrProAlaProAspAlaProLeuLys 182

QY 567 GTCTCTGACTTTGGCCTGTCTCCAAAATACAAGCTGGCAACATGCTA---GGCACAGCCTGT 623

Db 183 IleAlaAspPheGlyLeuSerLysIleValGluHisGlnValLeuMetLysThrValCys 202

QY 624 GGGACCCAGGATATGFGCCCCAGAGCTCCTGGAGCAGAAACCCTACGGGAAGGCCGTA 683

Db 203 GlyThrProGlyTyrCysAlaProGluIleLeuArgGlyCysAlaTyrGlyProGluVal 222

QY 684 GATGTGTGGCCCTGGGTGTCTATCTCCTACATCCTCGTGTGTGGGTACCCCCCTCTCTAT 743

Db 223 AspMetTrpSerValGlyIleIleThrTyrIleLeuLeuCysGlyPheGluProPheTyr 242

QY 744 GATGAG---AGCGATCCTGAACCTCTTCAGCCAGATCTTGAGGGCCAGCTATGAGTTTGAC 800

Db 243 AspGluArgGlyAspGlnPheMetPheArgArgIleLeuAsnCysGluTyrTyrPheIle 262

QY 801 TCCCCCTTTTGGGATGACATCTCAGAATCAGCCAAAGACTTCATTCCGCCACCTTCTGGAA 860

Db 263 SerProTrpTrpAspGluValSerLeuAlaLysAspLeuValArgLysLeuIleVal 282

QY 861 CGTGATCCCCAGAGGTTCACTGCCAGCGCCCTACAGCATCTTTGGATCTCTGGG 920

Db 283 LeuAspProLysLysArgLeuThrThrPheGlnAlaLeuGlnHisProTrpValThrGly 302

QY 921 GATGCAGCCTTCGATAGGACATCCTGGGTTCTGTCTGTGAGCAGATCCAGAGAATTTT 980

Db 303 LysAlaAla---AsnPheValHisMetAspThrAlaGlnLysLysLeuGlnGluPheAsn 321

QY 981 GCCAGGACCCACTGGAAGCGTGCATTCATGCCACATCATTCCTACGTACATCCGTAAG 1040

Db 322 AlaArgArgLysLeuLysAlaAlaValLysAlaVal----- 333

QY 1041 CTGGGACAAAGCCCAGAGGTGAGGAGGCTCCAGGAGGTGTATGACCCGTATAGCCAC 1100

Db 334 ValAlaSerSerArgLeuGlySerAlaSerSerHisGlySerIleGlnGluSerHis 353

RESULT 6

TVRTC4

Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) IV - rat

N;Alternate names: Ca2+/calmodulin-dependent protein kinase Gr

N;Contains: calspermin

C;Species: Rattus norvegicus (Norway rat)

C;Date: 31-Mar-1993 #sequence\_revision 31-Mar-1993 #text\_change 09-Jul-2004

C;Accession: A41103; A41237; A32865; A41250; A32035; A60255; I53706

R;Ohmstede, C.A.; Bland, M.M.; Merrill, B.M.; Sahyoun, N.

Proc. Natl. Acad. Sci. U.S.A. 88, 5784-5788, 1991

A;Title: Relationship of genes encoding Ca(2+)/calmodulin-dependent protein kinase Gr an

A;Reference number: A41103; PMID:91288548; PMID:1648230

A;Accession: A41103

A;Molecule type: DNA

A;Residues: 47-141,'NE',144-474 <OH1>

A;Cross-references: UNIPROT:P13234; GB:M74488; NID:G203219; PIDN:AAA40845.1; PID:G20322

A;Note: this sequence has been revised in reference A41237

R;Ohmstede, C.A.; Bland, M.M.; Merrill, B.M.; Sahyoun, N.

Proc. Natl. Acad. Sci. U.S.A. 88, 9375, 1991

A;Reference number: A41237

A;Accession: A41237

A;Molecule type: DNA

A;Residues: 142-143 <OH2>

A;Cross-references: GB:M63334

A;Note: this is a revision to the sequence from reference A41103

R;Ohmstede, C.A.; Jensen, K.F.; Sahyoun, N.E.

J. Biol. Chem. 264, 5866-5875, 1989

A;Title: Ca(2+)/calmodulin-dependent protein kinase enriched in cerebellar granule cell

A;Reference number: A32865; MUID:89174647; PMID:2538431

A;Accession: A32865

A;Molecule type: mRNA

A;Residues: 250-474 <OH3>

A;Cross-references: GB:J04600; NID:G206172; PIDN:AAA41867.1; PID:G206173

R;Means, A.R.; Cruzalegui, F.; LeMagueresse, B.; Needleman, D.S.; Slaughte, G.R.; Ono,

Mol. Cell. Biol. 11, 3960-3971, 1991

A;Title: A novel Ca(2+)/calmodulin-dependent protein kinase and a male germ cell-specif

A;Reference number: A41250; MUID:91304387; PMID:1649385

A;Accession: A41250

A;Molecule type: mRNA

A;Residues: 1-371,'M',373-408,'Q',410-474 <MEA>

A;Cross-references: GB:M64757

R;Ono, T.; Slaughte, G.R.; Cook, R.G.; Means, A.R.

J. Biol. Chem. 264, 2081-2087, 1989

A;Title: Molecular cloning sequence and distribution of rat calspermin, a high affinity

A;Reference number: A32035; MUID:89123272; PMID:2914893

A;Accession: A32035

A;Molecule type: mRNA

A;Residues: 306-371,'M',373-474 <ON1>

A;Cross-references: GB:J04446; NID:G203642; PIDN:AAA40990.1; PID:G203643

R;Ono, T.; Means, A.R.

Adv. Exp. Med. Biol. 255, 263-268, 1989

A;Title: Calspermin is a testis specific calmodulin-binding protein closely related to

A;Reference number: A60255; MUID:90144189; PMID:2618865

A;Accession: A60255

A;Molecule type: protein

A;Residues: 335-363 <ON2>

A;Note: the amino end of calspermin was blocked

R;Bland, M.M.

Gene 137, 351-352, 1993

A;Title: Identification of alternate 5' untranslated regions in the gene encoding Ca2+/-

A;Reference number: I53706; MUID:94131312; PMID:8299971

A;Accession: I53706

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-37 <RES>

A;Cross-references: GB:L16999; NID:G310086; PIDN:AAA17443.1; PID:G310087

C;Comment: Ca2+/calmodulin-dependent protein kinase IV is enriched in cerebellar granu

und in sperm cells.

C;Superfamily: Ca2+/calmodulin-dependent protein kinase; protein kinase homology

C;Keywords: alternative splicing; ATP; calmodulin binding; phosphotransferase; serine/t

F;40-296/Domain: protein kinase homology <KIN>

F;48-57/Region: protein kinase ATP-binding motif

F;306-474/Product: calspermin #status predicted <CSP>

F;318-337/Region: calmodulin binding #status predicted

F;71/Active site: Lys #status predicted

Alignment Scores:

Pred. No.:	1.09e-24	Length:	474
Score:	724.50	Matches:	156
Percent Similarity:	62.88%	Conservative:	71
Best Local Similarity:	43.21%	Mismatches:	118
Query Match:	25.23%	Indels:	16
DB:	1	Gaps:	6

US-10-032-254A-1 (1-1554) x TVRTC4 (1-474)

QY 96 GTCGCAGACATGCTGCTCAAGAAACAGACGGAGGACATCAGCAGTGTCTATGAGATC 155

Db 25 ValProAspTyrTrpIleAspGlySerLysArgAspProLeuSerAspPheGluVal 44  
QY 156 CGGAGAAAGCTGGGTCGGGTGCCTTCTCTGAGTGATGCTGGCCACAGAAAGGGGCTCT 215  
Db 45 GluSerGluLeuGlyArgGlyAlaThrSerIleValTyrArgCysLysGlnLysGlyThr 64  
QY 216 GCTCATCTTGTGGCCCTCAAGTGCATTCCCAAGAAAGCACCTTCGGGGCAGGAGGCCCTG 275  
Db 65 GlnLysProTyrAlaLeuLysValLeuLysLysThrVal-----AspLysLysIle 81  
QY 276 GTGGAGAAATGAGATCGCGGTACTTCGCAGAAATCAGCCATCCCAACATTGTGGCTCTGGAG 335  
Db 82 ValArgThrGluIleGlyValLeuLeuArgLeuSerHisProAsnIleIleLysLeuLys 101  
QY 336 GACGTCCATGAGAGTCCTTCTCATCTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAA 395  
Db 102 GluIlePheGluThrProThrGluIleSerLeuValLeuGluLeuValThrGlyGlyGlu 121  
QY 396 CTGTTTGACCGCATCATGGAGCGGGCTCCTACACAGAGAAGGACGCCAGCCACCTTGTA 455  
Db 122 LeuPheAspArgIleValGluLysGlyTyrTyrSerGluArgAspAlaAlaAspAlaVal 141  
QY 456 GGGCAGGTCCTTGGGCTGTCTCTACCTTCATAGCCTGGGCATCGTGCAACCGGGACCTC 515  
Db 142 LysGlnIleLeuGluAlaValAlaTyrLeuHisGluAsnGlyIleValHisArgAspLeu 161  
QY 516 AAGCCTGAAACCTCTCTATGCCACACACCTTTTGAGGACTCCAAGATCATGCTCTCTGAC 575  
Db 162 LysProGluAsnLeuLeuTyrAlaThrProAlaProAspAlaProLeuLysIleAlaAsp 181  
QY 576 TTTGGCCTGTCCAAATACAAAGCTGGCAACATGCTA---GGCACAGCCTGTGGGACCCCA 632  
Db 182 PheGlyLeuSerLysIleValGluHisGlnValLeuMetLysThrValCysGlyThrPro 201  
QY 633 GGATATGTGGCCCCAGAGCTCTGGAGCAGAAACCTACGGGAAGGCCGTAGATGTGTGG 692  
Db 202 GlyTyrCysAlaProGluIleLeuArgGlyCysAlaTyrGlyProGluValAspMetTrp 221  
QY 693 GCCCTGGGTGCATCTCCTPACATCCTGCTGTGGTACCCCCCTTCTCTATGATGAG--- 749  
Db 222 SerValGlyIleIleThrTyrIleLeuLeuCysGlyPheGluProPheTyrAspGluArg 241  
QY 750 AGCGATCCTGAACCTTCAGCCAGATTCTGAGGGCCAGCTATGAGTTTGACTCCCCCTTT 809  
Db 242 GlyAspGlnPheMetPheArgArgIleLeuAsnCysGluTyrTyrPheIleSerProTrp 261  
QY 810 TGGGATGACATCTCAGAAATCAGCCAAAGACTTCATTGCCACCTTCTGGAACGTGATCCC 869  
Db 262 TrpAspGluValSerLeuAsnAlaLysAspLeuValLysLysLeuIleValLeuAspPro 281  
QY 870 CAGAAAGAGGTTACCTGCCAGCAGGCCCTACAGCATCTTTGGATCTCTGGGGATGCAGCC 929  
Db 282 LysLysArgLeuThrThrPheGlnAlaLeuGlnHisProTrpValThrGlyLysAlaAla 301  
QY 930 TTCGATAGGGACATCCTGGGTTCTGTCAGTGAGCAGATCCAGAAGAAATTTTGCCAGGACC 989  
Db 302 ---AsnPheValHisMetAspThrAlaGlnLysLysLeuGlnGluPheAsnAlaArgArg 320  
QY 990 CACTGGAAGCGTGCATTCAATGCCACATCATTCCTACGTACATCCGTAGCTGGGACAA 1049  
Db 321 LysLeuLysAlaAlaValLysAlaVal-----ValAlaSer 332  
QY 1050 AGCCACAGGGGTGAGGCGCTCCAGGCAGTGATGACCCGTATAGCCCGTCATAGCCACCCAGGCCCTT 1109  
Db 333 SerArgLeuGlySerAlaSerSerSerHisThrAsnIleGlnGluSerAsn-LysAlaSe 352  
QY 1110 GGGACTAGCCAGTCCC---CCAAAGTGGTGAAACACAGGTAGATGCCAAGGAAGGCCAAGT 1166  
Db 352 rSerGluAlaGlnProAlaGlnAspGlyLysAspLysThrAspProLeuGluAsnLysII 372  
QY 1167 G 1167

Db 372 e 372  
RESULT 7  
I52637  
Ca2+/calmodulin-dependent protein kinase IV beta polypeptide - rat  
C;Species: Rattus sp. (rat)  
C;Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I52637  
R;Sakagami, H.; Kondo, H.  
Brain Res. Mol. Brain Res. 19, 215-218, 1993  
A;Title: Cloning and sequencing of a gene encoding the beta polypeptide of Ca2+/calmodu  
A;Reference number: I52637; MUID:94018484; PMID:8412563  
A;Accession: I52637  
A;Status: preliminary; translated from GB/EMBL/DBBJ  
A;Molecule type: mRNA  
A;Residues: 1-502 <RES>  
A;Cross-references: UNIPROT:Q63892; GB:S65840; NID:g425383; PIDN:AAH28372.1; PID:g42538  
C;Superfamily: Ca2+/calmodulin-dependent protein kinase; protein kinase homology  
C;Keywords: ATP; calmodulin binding  
F;68-324/Domain: protein kinase homology <KIN>  
F;76-84/Region: protein kinase ATP-binding motif  
  
Alignment Scores:  
Pred. No.: 1.32e-24 Length: 502  
Score: 722.50 Matches: 156  
Percent Similarity: 62.88% Conservative: 71  
Best Local Similarity: 43.21% Mismatches: 118  
Query Match: 25.16% Indels: 16  
DB: 2 Gaps: 6  
  
US-10-032-254A-1 (1-1554) x I52637 (1-502)  
  
QY 96 GTCGCAGACATGCTGCTGCTCAAGAAACAGACGAGGACATCAGCAGTGTCTATGAGATC 155  
Db 53 ValProAspTyrTrpIleAspGlySerLysArgAspProLeuSerAspPheGluVal 72  
QY 156 CGGAGAAAGCTGGGTCGGGTGCCTTCTCTGAGTGATGCTGGCCACGAAAGGGGCTCT 215  
Db 73 GluSerGluLeuGlyArgGlyAlaThrSerIleValTyrArgCysLysGlnLysGlyThr 92  
QY 216 GCTCATCTTGTGGCCCTCAAGTGCATTCCCAAGAAAGCACCTTCGGGGCAAGGAGGCCCTG 275  
Db 93 GlnLysProTyrAlaLeuLysValLeuLysLysThrVal-----AspLysLysIle 109  
QY 276 GTGGAGAAATGAGATCGCGGTACTTCGCAGAAATCAGCCATCCCAACATTGTGGCTCTGGAG 335  
Db 110 ValArgThrGluIleGlyValLeuLeuArgLeuSerHisProAsnIleIleLysLeuLys 129  
QY 336 GACGTCCATGAGAGTCCTTCTCATCTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAA 395  
Db 130 GluIlePheGluThrProThrGluIleSerLeuValLeuGluLeuValThrGlyGlyGlu 149  
QY 396 CTGTTTGACCGCATCATGGAGCGGGCTCCTACACAGAGAAGGACGCCACCTTGTA 455  
Db 150 LeuPheAspArgIleValGluLysGlyTyrTyrSerGluArgAspAlaAlaAspAlaVal 169  
QY 456 GGGCAGGTCCTTGGCGCTGTCTCCTACCTTACCTTATAGCCTGGGCATCGTGCCACCGGGACCTC 515  
Db 170 LysGlnIleLeuGluAlaValAlaTyrLeuHisGluAsnGlyIleValHisArgAspLeu 189  
QY 516 AAGCCTGAAACCTCTCTATGCCACACCTTTTGAGGACTCCAAGATCATGTTCTCTGAC 575  
Db 190 LysProGluAsnLeuLeuTyrAlaThrProAlaProAspAlaProLeuLysIleAlaAsp 209  
QY 576 TTTGGCCTGTCCAAATAACAAGCTGGCAACATGCTA---GGCACAGCCTGTGGGACCCCA 632  
Db 210 PheGlyLeuSerLysIleValGluHisGlnValLeuMetLysThrValCysGlyThrPro 229  
QY 633 GGATATGTGGCCCCAGAGCTCTCTGGAGCAGAAACCTACGGGAAGGCCGTAGATGTGTGG 692  
Db 230 GlyTyrCysAlaProGluIleLeuArgGlyCysAlaTyrGlyProGluValAspMetTrp 249  
QY 693 GCCCTGGGTGCATCTCCTACATCCTTGCTGTGGGTACCCCTTCTATGATGAG--- 749



Db 250 SerValGlyIleThrTyrlleLeuLeuCysGlyPheGluProPheTyrAspGluArg 269  
QY 750 AGGATCCTGAACCTCTTCCAGCCAGATCTTGAGGGCCAGCTATGAGTTTGACTCCCCCTTT 809  
Db 270 GlyAspGlnPheMetPheArgIleLeuAsnCysGluTyrTyrPheIleSerProTrp 289  
QY 810 TGGGATGACATCTCAGAAATCAGCAAAAGACTTTCATTCGCCACCTTCTGGAACGTGATCCC 869  
Db 290 TrpAspGluValSerLeuAsnAlaLysAspLeuValLysLysLeuIleValLeuAspPro 309  
QY 870 CAGAAGAGGTTACCTGCCAGGCGCCTACAGCATCTTTGGATCTCTGGGGATGCAGCC 929  
Db 310 LysLysArgLeuThrThrPheGlnAlaLeuGlnHisProTrpValThrGlyLysAlaAla 329  
QY 930 TTCGATAGGGACATCCTGGGTTCTGTCAGTGAGCAGATCCAGAAGAATTTTGGCAGGACC 989  
Db 330 ---AsnPheValHisMetAspThrAlaGlnLysLysLeuGlnGluPheAsnAlaArgArg 348  
QY 990 CACTGGAAGCGTGCAATTCATGCGCACATCATTCCTACGTACATCCGTAAGCTGGGACAA 1049  
Db 349 LysLeuLysAlaAlaValLysAlaVal-----ValAlaSer 360  
QY 1050 AGCCAGAGGGTGAGGAGGCGCTCCAGGCAGTGATGACCGTCATAGCCACCCAGGCCCTT 1109  
Db 361 SerArgLeuGlySerAlaSerSerHisThrAsnIleGlnGluSerAsn-LysAlaSe 380  
QY 1110 GGGACTAGCCAGTCCC---CCAAGTGGTGAAACCAGGTAGATGCCAAGGAAGGCCAAGT 1166  
Db 380 rSerGluAlaGlnProAlaGlnAspGlyLysAspLysThrAspProLeuGluAsnLysMe 400  
QY 1167 G.1167  
Db 400 t.400  
RESULT 8  
S17656  
Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) IV - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: S17656; A29878; I49571  
R;Jones, D.A.; Glod, J.; Wilson-Shaw, D.; Hahn, W.E.; Sikela, J.M.  
FEBS Lett. 289, 105-109, 1991  
A;Title: cDNA sequence and differential expression of the mouse Ca (2+)/calmodulin-depend  
A;Reference number: S17656; MUID:91372388; PMID:18933997  
A;Accession: S17656  
A;Molecule type: mRNA  
A;Residues: 1-469 <JON>  
A;Cross-references: UNIPROT:P08414; EMBL:X58995; NID:g50366; PIDN:CAA41741.1; PID:g50367  
R;Sikela, J.M.; Hahn, W.E.  
Proc. Natl. Acad. Sci. U.S.A. 84, 3038-3042, 1987  
A;Title: Screening an expression library with a ligand probe: isolation and sequence of  
A;Reference number: A29878; MUID:87204263; PMID:3033675  
A;Accession: A29878  
A;Molecule type: mRNA  
A;Residues: 315-469 <SIK>  
A;Cross-references: GB:M16206; NID:g200360; PIDN:AAA39933.1; PID:g387512  
R;Sikela, J.M.; Law, M.L.; Kao, F.  
Genomics 4, 21-27, 1989  
A;Title: Chromosomal localization of the human gene for brain Ca2+/calmodulin-dependent  
A;Reference number: I49571; MUID:89122027; PMID:2536634  
A;Accession: I49571  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 250-277, 'CFGI', 281-301, 'T', 303-338, 'X', 340-469 <RES>  
A;Cross-references: GB:J03057; NID:g192366; PIDN:AAA37366.1; PID:g192367  
A;Experimental source: brain  
C;Superfamily: Ca2+/calmodulin-dependent protein kinase; protein kinase homology  
C;Keywords: alternative splicing; Arp; calmodulin binding; phosphotransferase; serine/th  
F;40-296/Domain: protein kinase homology <KIN>  
F;48-56/Region: protein kinase ATP-binding motif  
F;306-469/Product: calspermin #status predicted <CSP>  
F;318-337/Region: calmodulin binding #status predicted

F;71/Active site: Lys #status predicted  
Alignment Scores:  
Pred. No.: 1.89e-24 Length: 469  
Score: 719.00 Matches: 154  
Percent Similarity: 62.46% Conservative: 69  
Best Local Similarity: 43.14% Mismatches: 117  
Query Match: 25.03% Indels: 17  
DB: 1 Gaps: 6  
US-10-032-254A-1 (1-1554) x S17656 (1-469)  
QY 96 GTCGCAGACATGCTGCTGCTCAAGAAACAGACGAGGAGCATCAGCAGTGTCTATGAGATC 155  
Db 25 ValProAspTyrTrpIleAspGlySerAsnArgAspProLeuGlyAspPhePheGluVal 44  
QY 156 CGGAGAAAGCTGGGCTCGGCTGCCCTTCTCTGAGGTGATGCTGGCCCGAGAAAGGGCTCT 215  
Db 45 GluSerGluLeuGlyArgGlyAlaThrSerIleValTyrArgCysLysGlnLysGlyThr 64  
QY 216 GCTCATCTTGTGGCCCTCAAGTGCATTCCTCCCAAGAAAGCACTTCGGGGCAAGGAGGCCCTG 275  
Db 65 GlnLysProTyrAlaLeuLysValLeuLysLysThrVal-----AspLysLysIle 81  
QY 276 GTGGAGAATGAGATCGCGTACTTTCGAGAATCAGCCATCCCAACATTTGTGGCTCTGGAG 335  
Db 82 ValArgThrGluIleGlyValLeuLeuArgLeuSerHisProAsnIleIleLysLeuLys 101  
QY 336 GACGTCCATGAGATCCTTCTCATCTCTACTTGGCCATCGAGCTGGTAACAGGTGTTGTA 455  
Db 102 GluIlePheGluThrProThrGluIleSerLeuValLeuGluLeuValThrGlyGlyGlu 121  
QY 396 CTGTTTGACCGCATCATGGAGCGGGGCTCTCTACCTTACCTGCGCATCGTGGCATCGTGCACCGGACCTC 515  
Db 142 LysGlnIleLeuGluAlaValAlaTyrLeuHisGluAsnGlyIleValHisArgAspLeu 161  
QY 516 AAGCCTGAAACCTCCTCTATGCCACACCTTTTGGAGGACTCCAAAGATCATGGTCTCTGAC 575  
Db 162 LysProGluAsnLeuLeuTyrAlaThrProAlaProAspAlaProLeuLysIleAlaAsp 181  
QY 576 TTTGGCCTGTCCAAATACAAGCTGGCAACATGTCTA---GGCACAGCCTGTGGGACCCCA 632  
Db 182 PheGlyLeuSerLysIleValGluHisGlnValLeuMetLysThrValCysGlyThrPro 201  
QY 633 GGATATGTGGCCCCAGAGTCTCTGGAGCAGAAACCTTACGGGAAGCCGTAGATGTGTGG 692  
Db 202 GlyTyrCysAlaProGluIleLeuArgGlyCysAlaTyrGlyProGluValAspMetTrp 221  
QY 693 GCCCTGGGTGTCATCTCTACATCCTGTGTGTGGGTACCCCTTCTATGATGAG--- 749  
Db 222 SerValGlyIleIleThrTyrIleLeuLeuCysGlyPheGluProPheTyrAspGluArg 241  
QY 750 AGCGATCCTGAACCTTTCAGCCAGATTTCTGAGGGCCAGCTATGAGTTTGACTCCCCCTTT 809  
Db 242 GlyAspGlnPheMetPheArgArgIleLeuAsnCysGluTyrTyrPheIleSerProTrp 261  
QY 810 TGGGATGACATCTCAGAAATCAGCCAAAGACTTTCATTCGCCACCTTCTTGGATCTCTGGGATGCAGCC 869  
Db 262 TrpAspGluValSerLeuAsnAlaLysAspLeuValLysLysLeuIleValLeuAspPro 281  
QY 870 CAGAAGAGGTTTACCTGCCAGGCGCCTACAGCATCTTTGGATCTCTGGGATGCAGCC 929  
Db 282 LysLysArgLeuThrThrPheGlnAlaLeuGlnHisProTrpValThrGlyLysAlaAla 301  
QY 930 TTCGATAGGGACATCCTGGGTTCTGTTCAGTGAGCAGATCCAGAAGAATTTTGGCAGGACC 989  
Db 302 ---AsnPheValHisMetAspThrAlaGlnLysLysLeuGlnGluPheAsnAlaArgArg 320  
QY 990 CACTGGAAGCGTGCAATTCATGCGCACATCATTCCTACGTACATCCGTAAGCTGGGACAA 1049

Db 321 LysLeuLysAlaAlaValLysAlaVal-----ValAlaSer 332

QY 1050 AGCCAGAGGTGAGGAGGCTCCAGGCAGTGATGACCCGTATAGCCACCCAGGCCTT 1109

Db 333 SerArgLeuGlySerAlaSerSerHisThrSerIleGlnGluAsnHis--LysAla-- 351

QY 1110 GGGACTAGCCAGTCCCCCAAGTGGTGAACACCCAGGTAGATGCCAAGGAA 1158

Db 352 ----SerSerAspProProSerThrGlnAspAlaLysAspSerThrAsp 366

RESULT 9

I56542

calmodulin-binding protein - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 26-Jul-1996 #sequence\_revision 26-Jul-1996 #text\_change 16-Aug-2004

C;Accession: I56542

R;Godbout, M.; Erlander, M.G.; Hasel, K.W.; Danielson, P.E.; Wong, K.K.; Battenberg, E.L

J. Neurosci. 14, 1-13, 1994

A;Title: IGS: a calmodulin-binding, vesicle-associated, protein kinase-like protein enri

A;Reference number: I56542; MUID:94110847; PMID:8283228

A;Accession: I56542

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-504 <RES>

A;Cross-references: UNIPROT:Q63092; GB:L22557; NID:g349074; PIDN:AAA16633.1; PID:g349075

C;Superfamily: protein kinase homology

C;Keywords: calmodulin binding

F;22-286/Domain: protein kinase homology <KIN>

Alignment Scores:

Pred. No.:	2.28e-24	Length:	504
Score:	717.00	Matches:	154
Percent Similarity:	59.18%	Conservative:	78
Best Local Similarity:	39.29%	Mismatches:	131
Query Match:	24.97%	Indels:	29
DB:	2	Gaps:	5

US-10-032-254A-1 (1-1554) x I56542 (1-504)

QY 123 CAGACGGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAAGCTGGGCTCGGTCCTTC 182

Db 16 GlnProSerGluValThrAspArgTyrAspLeuGlyGlnValLysThrGluGluPhe 35

QY 183 TCTGAGGTGATGCTGGCCACAGAAAGGGCTCTGCTCATCTTGTGGCCCTCAAGTGCATT 242

Db 36 CysGluIlePheArgAlaLysAspLysThrThrGlyLysLeuHisThrCysLysLysPhe 55

QY 243 CCCAAGAAAGCACTTCGGGGCAAGGAGGCCCTGGTGGAGAATGAGATCGCGTACTTCGC 302

Db 56 GlnLysArgAspGlyArgLysValArgLysAlaAlaLysAsnGluIleGlyIleLeuLys 75

QY 303 AGAATCAGCCATCCCAACATTGTGGCTCTGGAGGAGCTCCATGAGAGTCCCTCTCATCTC 362

Db 76 MetValLysHisProAsnIleLeuGlnLeuValAspValPheValThrArgLysGluTyr 95

QY 363 TACTTGGCCATGGAGCTGGTAACAGGTGGTGAACCTGTTGACCCGCATCATGGACGGGC 422

Db 96 PheIlePheLeuGluLeuAlaThrGlyArgGluValPheAspTrpIleLeuAspGlnGly 115

QY 423 TCCTACACAGAGGAGGCCAGCCACCTTGTAGGCGAGGTCTCTGGCGTGTCTCCTAC 482

Db 116 TyrTyrSerGluArgAspThrSerAsnValValArgGlnValLeuGluAlaValAlaTyr 135

QY 483 CTTTCATAGCCTGGGCATCGTCACCGGACCTCAAGCCTGAAAACCTCCTCTATGCCACA 542

Db 136 LeuHisSerLeuLysIleValHisArgAsnLeuLysLeuGluAsnLeuValTyrTyrAsn 155

QY 543 CCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTGGCCTGTCCAAAATACAAGCTGGC 602

Db 156 ArgLeuLysAsnSerLysIleValIleSerAspPheHisLeuAlaLysLeuGluAsnGly 175

QY 603 AACATGCTAGGCACAGCCTGTGGGACCCAGGATATGTGGCCCCAGAGCTCTCTGGAGCAG 662

Db 176 ---LeuIleLysGluProCysGlyThrProGluTyrLeuAlaProGluValValGlyArg 194

QY 663 AAACCTACGGGAAGCGGTAGATGTGTGGGCCCTTGGGTGTCACTCTCTACATCCTGCTG 722

Db 195 GlnArgTyrGlyArgProValAspCysTrpAlaIleGlyValIleMetTyrIleLeuLeu 214

QY 723 TGTGGGTACCCCCCTTCTATGATGAG-----ACCGATCCT 758

Db 215 SerGlyAsnProProPheTyrGluGluValGluGluAspTyrGluAsnHisAspLys 234

QY 759 GAACTCTTCAGCCAGATTCTGAGGGCCAGCTATGAGTTTGACTCCCCCTTTTGGGATGAC 818

Db 235 AsnLeuPheArgLysIleLeuAlaGlyAspTyrGluPheAspSerProTyrTrpAspAsp 254

QY 819 ATCTCAGAATCAGCCAAAGACTTTCATTCCGCACCTTCTGGAACGTGATCCCCAGAAAGG 878

Db 255 IleSerGlnAlaAlaLysAspLeuValThrArgLeuMetGluValGluGlnAspGlnArg 274

QY 879 TTCACCTGCCAGCAGCCCTACAGCATCTTTGGATCTCTGGGGATGCAGCCTTCGATAGG 938

Db 275 IleThrAlaGluGluAlaIleSerHisGluTrpIleSerGlyAsnAlaAlaSerAspLys 294

QY 939 GACATCCTGGGTTCTGTGAGTGAGCAGATCCAGAAAGAAATTTTGCAGGACCCACTGGAAG 998

Db 295 AsnIleLysAspGlyValCysAlaGlnIleGluLysAsnPheAlaArgAlaLysTrpLys 314

QY 999 CGTGCATTCAATGCCACATCATCTTCTACGTACATCCGTAAGCTGGGACAAAGC----- 1052

Db 315 LysAlaValArgValThrThrLeuMetLysArgLeuArgAlaProGluGlnSerGlyThr 334

QY 1053 -----CCAGAGGGTGAGGAGGCCCTCCAGGCAGTGATGACCCGTCATAGCCACCCAGGC 1106

Db 335 AlaAlaThrSerAspAlaAlaThr-ProGlyAlaAlaGlyGlyAlaValAlaAla---Al 353

QY 1107 CTTGGGACTAGCCAGTCCCCCAAGTGGTGAACACCAAGGTAGATGCCAAGGAAGGCCAAGT 1166

Db 353 aAlaGlyGlyAlaAlaProAlaSerGlyAlaSerAlaThrValGlyThrGlyGlyAspAl 373

QY 1167 GGACTGACTCCCGGTTTTTCTTCTCCTCCAGCCCTTTTGGTCTCTTCTCTGGATCCTGTG 1226

Db 373 agly-----CysAlaAlaLysSe 379

QY 1227 CTCCAGACTGGCCTCTGCTGGAAGTCTGAGACT 1260

Db 379 rAspAspMetalaSerAlaAspArgSerAlaThr 390

RESULT 10

T30814

calmodulin-binding protein kinase - Fugu rubripes

C;Species: Fugu rubripes

C;Date: 02-Sep-2000 #sequence\_revision 02-Sep-2000 #text\_change 09-Jul-2004

C;Accession: T30814

R;Cottage, A.J.; Clark, M.; Hawker, K.; Umrانيا, Y.; Wheller, D.; Bishop, M.; Elgar, G.

FEBS Lett. 443, 370-374, 1999

A;Title: Three receptor genes for plasminogen related growth factors in the genome of t

A;Reference number: Z20880; MUID:99148833; PMID:10025966

A;Accession: T30814

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-421 <COT>

A;Cross-references: UNIPROT:Q9YGM4; EMBL:AJ010348; NID:e1355080; PID:e1355083; PIDN:CAA

C;Genetics:

A;Introns: 32/2; 76/2; 101/2; 147/3; 186/1; 211/2; 257/1; 283/2; 312/3

Alignment Scores:

Pred. No.:	7.81e-24	Length:	421
Score:	705.00	Matches:	147
Percent Similarity:	59.12%	Conservative:	67
Best Local Similarity:	40.61%	Mismatches:	116
Query Match:	24.55%	Indels:	32
DB:	2	Gaps:	5





Db	102	TyrSerGluAlaAspAlaAlaAsnLeuValLysLysIleValSerAlaValGlyTyrLeu	121	:     :     :     :     :     :     :
QY	486	CATAGCCTGGGCATCGTGACCGGGACCTCAAGCCTGAAAAACCTCCTCTATGCCACACCT	545	:     :     :     :     :     :     :
Db	122	HisGlyLeuAsnIleValHisArgAspLeuLysProGluAsnLeuLeuLysSerLys	141	:     :     :     :     :     :     :
QY	546	TTTGAGGACTCCAAGATCATGGTCTCTGACTTTGGCCTGTCCAAAATACAGCTGGCAAC	605	:     :     :     :     :     :     :
Db	142	GluAsnHisLeuGluValAlaIleAlaAspPheGlyLeuSerLysIlelleGlyGlnThr	161	:     :     :     :     :     :     :
QY	606	ATG---CTAGGCACAGCCTGTGGGACCCACGATATGTGGCCCCCAGAGCTCCTGGAGCAG	662	:     :     :     :     :     :     :
Db	162	LeuValMetGlnThrAlaCysGlyThrProSerTyrValAlaProGluValLeuAsnAla	181	:     :     :     :     :     :     :
QY	663	AAACCCCTACGGGAAGCGCGTAGATGTGTGGGCCCTGGCTCATCTCCTACATCCTGCTG	722	:     :     :     :     :     :     :
Db	182	ThrGlyTyrAspLysGluValAspMetTrpSerIleGlyValIleThrTyrIleLeuLeu	201	:     :     :     :     :     :     :
QY	723	TGTGGGTACCCCTTCTATGATGAGAGCGATCCTGAACTCTTCAGCCAGATTCTGAGG	782	:     :     :     :     :     :     :
Db	202	CysGlyPheProProPheTyrGlyAspThrValProGluIlePheGluGlnIleMetGlu	221	:     :     :     :     :     :     :
QY	783	GCCAGCTATGAGTTTGACTCCCCCTTTTGGGATGACATCTCAGAATCAGCCAAAGACTTC	842	:     :     :     :     :     :     :
Db	222	ValAsnTyrGluPheProGluGluTyrTrpGlyGlyIleSerLysGluAlaLysAspPhe	241	:     :     :     :     :     :     :
QY	843	ATTGCGCCACCTTCTGGAACGTGATCCCCAGAGAGGTTACCTGCCAGCAGCCCTACAG	902	:     :     :     :     :     :     :
Db	242	IleGlyLysLeuLeuValValAspValSerLysArgLeuAsnAlaThrAsnAlaLeuAsn	261	:     :     :     :     :     :     :
QY	903	CATCTTTGGATCTCTGGGATGCAGCCTTCGATAGGACATCCTGGGTTCTGTCAGTGAG	962	:     :     :     :     :     :     :
Db	262	HisProTrpLeuLysSerAsnAsnSerAsnAsnThrIleAspThrValLysMetLysGlu	281	:     :     :     :     :     :     :
QY	963	CAGATC-----CAGAAGAATTTTGCCAGGACCCACTGG-----AAGCGTCATTC	1007	:     :     :     :     :     :     :
Db	282	TyrIleValGluArgArgLysAsn--SerAsnGluAsnTrpLeuThrLysArgIlePhe	300	:     :     :     :     :     :     :
RESULT 12				
JN0323				
Ca2+/calmodulin-dependent protein kinase (EC 2.7.1.123) - Emericella nidulans				
C;Species: Emericella nidulans, Aspergillus nidulans				
C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 16-Aug-2004				
C;Accession: JN0323				
R;Kornstein, L.B.; Gaiso, M.L.; Hammell, R.L.; Bartelt, D.C.				
Gene 113, 75-82, 1992				
A;Title: Cloning and sequence determination of a cDNA encoding Aspergillus nidulans calmodulin-dependent protein kinase				
A;Reference number: JN0323; MUID:92225350; PMID:1563634				
A;Accession: JN0323				
A;Molecule type: mRNA				
A;Residues: 1-414 <KOR>				
A;Cross-references: UNIPROT:Q00771; GB:M74120; NID:g2804304; PIDN:AAB97502.1; PID:g16803				
C;Comment: This protein has been implicated in cellular signal transduction and cell division				
C;Superfamily: protein kinase homology				
C;Keywords: ATP; calmodulin binding; phosphotransferase				
F;21-278/Domain: protein kinase homology <KIN>				
F;29-37/Region: protein kinase ATP-binding motif				
F;232-315/Region: calmodulin binding #status predicted				
Alignment Scores:				
Pred. No.:	2.54e-21	Length:	414	
Score:	647.00	Matches:	150	
Percent Similarity:	56.88%	Conservative:	65	
Best Local Similarity:	39.68%	Mismatches:	130	
Query Match:	22.53%	Indels:	33	
DB:	2	Gaps:	6	
US-10-032-254A-1 (1-1554) x JN0323 (1-414)				
QY	141	ACTGTCATGAGATCCGGGAGAGAGCTGGGCTCGGGTGCTCTCTGAGGTGATGCTGGCC	200	:     :     :     :     :     :     :
Db	21	SerLeuTyrArgPheGlyArgThrLeuGlyAlaGlyThrTyrGlyIleValArgGluAla	40	:     :     :     :     :     :     :

QY	201	CAGGAAAGGGCTCTGCTCATCTTGTGGCCCTCAAGTGCATTCCTCCAAAGAAAGCACTTCGG	260	:     :     :     :     :     :     :
Db	41	Asp-----CysSerSerGlyLysValAlaValLysIleIleLeuLysArgAsnValArg	58	:     :     :     :     :     :     :
QY	261	GGCAAGGAGGCCCTGGTGGAGAATGAGATCGCGGTACTTCGCAGAATCAGCCATCCCAAC	320	:     :     :     :     :     :     :
Db	59	GlyAsnGluArgMetValTyrAspGluLeuAspLeuGlnLysLeuAsnHisProHis	78	:     :     :     :     :     :     :
QY	321	ATTGTGGCTCTGGAGGACGTCATGAGAGTCTCTCTCATCTCTACTTGGCCATGGAGCTG	380	:     :     :     :     :     :     :
Db	79	IleValHisPheValAspTrpPheGluSerLysAspLysPheTyrIleValThrGlnLeu	98	:     :     :     :     :     :     :
QY	381	GTAACAGGTGTGAACCTGTTTACCGCATCATGGAGCGGGCTCCTACACAGAGAGGAC	440	:     :     :     :     :     :     :
Db	99	AlaThrGlyGlyGluLeuPheAspArgIleCysGluTyrGlyLysPheThrGluLysAsp	118	:     :     :     :     :     :     :
QY	441	GCCAGCCACCTTGTAGGGCAGGTCTTGGCGTGTCTCTACCTTTCATAGCTGGGCATC	500	:     :     :     :     :     :     :
Db	119	AlaSerGlnThrIleArgGlnValLeuAspAlaValAsnTyrLeuHisGlnArgAsnIle	138	:     :     :     :     :     :     :
QY	501	GTGCACCGGGACCTCAAGCCTGAAACCTCCTCTATGCCACACCTTTTGGAGACTCCAAG	560	:     :     :     :     :     :     :
Db	139	ValHisArgAspLeuLysProGluAsnLeuLeuTyrLeuThrArgAspLeuAspSerGln	158	:     :     :     :     :     :     :
QY	561	ATCATGGTCTCTGACTTTGGCCTGTCCAAATA-----CAAGCTGGCAACATGCTAGGC	614	:     :     :     :     :     :     :
Db	159	LeuValLeuAlaAspPheGlyIleAlaLysMetLeuAspAsnProAlaGluValLeuThr	178	:     :     :     :     :     :     :
QY	615	ACAGCCTGTGGGACCCACAGGATATGTGGGCCCCACAGAGCTCCTGGAGCAGAAACCTACGGG	674	:     :     :     :     :     :     :
Db	179	SerMetAlaGlySerPheGlyTyrAlaAlaProGluValMetLeuLysGlnGlyHisGly	198	:     :     :     :     :     :     :
QY	675	AAGGCCGTAGATGTGTGGCCCTGGGTGTCTCTCTACATCCTGTGTGGTACCC	734	:     :     :     :     :     :     :
Db	199	LysAlaValAspIleTrpSerLeuGlyValIleThrTyrThrLeuLeuCysGlyTyrSer	218	:     :     :     :     :     :     :
QY	735	CCCTTCTATGATGAGAGCGATCCTGAACTCTTCAGCCAGATTCTGAGGGCCAGCTATGAG	794	:     :     :     :     :     :     :
Db	219	ProPheArgSerGluAsnLeuThrAspLeuIleGluGluCysArgSerGlyArgValVal	238	:     :     :     :     :     :     :
QY	795	TTTGACTCCCCCTTTTGGGATGACATCTCAGAATCAGCCAAAGACTTTCATTCGCCACCTT	854	:     :     :     :     :     :     :
Db	239	PheHisGluArgTyrTrpLysAspValSerLysAspAlaLysAspPheIleLeuSerLeu	258	:     :     :     :     :     :     :
QY	855	CTGGAACGTGATCCCCAGAAAGAGTTTCACCTGCCAGCAGGCCCTACAGCATCTTTGGATC	914	:     :     :     :     :     :     :
Db	259	LeuGlnValAspProAlaGlnArgProThrSerGluGluAlaLeuLysHisProTrpLeu	278	:     :     :     :     :     :     :
QY	915	TCTGGGGATGCAGCCTTCGATAGGACATCCTGGGTCTGTTCAGTGAGCAGATCCAGAAG	974	:     :     :     :     :     :     :
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QY	975	AATTTTGCAGGACCCACTGGAAGCGTGCAATTCATGCCACATCATTCCTACGTCACATC	1034	:     :     :     :     :     :     :
Db	295	TyrIleAlaArgSerArgLeuLysArgGlyIleGluIleLysLeuAlaAsnArgIle	314	:     :     :     :     :     :     :
QY	1035	CGTAAGCTGGGACAAAAGCCAGAGGGTGAGGAGGCTCCAGGCAGTGTATGACCGTCAT	1094	:     :     :     :     :     :     :
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QY	1095	AGCCACCCAGGCCCTTGGGACTAGCCAGTCCCCCAAGTGGTGAAACCAGGTAGATGCCAA	1154	:     :     :     :     :     :     :
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Db	344	-----LeuSerProPheProAlaLeuSe	351	:     :     :     :     :     :     :
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Db 190 ProTyrGlyLysSerValAspIleTrpAlaCysGlyValIleLeuTyrIleLeuVal 209  
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Db 285 GlnGluThrValAspCysLeuLysLysPheAsnAlaArgArgLysLeuLysGlyAlaIle 304  
QY 1008 AATGCCACA-----TCATTCTACGTACATCCGTAAGCTGGGA 1046  
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Job time : 63 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: June 5, 2005, 22:52:50 ; Search time 7779 Seconds  
(without alignments)  
7604.046 Million cell updates/sec

Title: US-10-032-254A-1  
Perfect score: 1554  
Sequence: 1 gttgcggagtcctccactc.....caaaaaaaaaaaaaaaaaa 1554

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_htc:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length	Description
1	995	64.0	AY418574 Mus muscu
2	830.8	53.5	CR611192 full-leng
3	823.2	53.0	CA978376 AGENCOURT
4	806.2	51.9	AY418572 Homo sapi
5	686.4	44.2	BU524572 AGENCOURT
6	682	43.9	BF582563 602094540
7	675	43.4	AY418573 Pan trogl
8	654.2	42.1	CB192924 AGENCOURT
9	646.2	41.6	AU079915 AU079915
10	636.2	40.9	AU080044 AU080044
11	633.8	40.8	CD776443 UI-M-AQ0-
12	628	40.4	BG695422 NISC iv17
13	625.2	40.2	BG702279 602683496
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15	622.6	40.1	BM986320 EST531228
16	615.4	39.6	BI756289 603024363
17	608.6	39.2	BG715227 602676104
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19	606.2	39.0	BQ066920 AGENCOURT
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21	601.4	38.7	BU525063 AGENCOURT
22	600.4	38.6	AU079926 AU079926
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24	582.8	37.5	BI824238 603040618

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	27	558.2	35.9	770	4	BI829739	BI829739 603079808
	28	548.4	35.3	706	4	BI668490	BI668490 603293766
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	30	534.8	34.4	857	4	BI545446	BI545446 603187596
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ALIGNMENTS

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DEFINITION Mus musculus HCM6602 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.  
ACCESSION AY418574  
VERSION AY418574.1 GI:39774534  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE 1 (bases 1 to 995)  
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 995)  
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
COMMENT These sequences were made by sequencing genomic exons and ordering them based on alignment.  
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gene  
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Best Local Similarity 100.0%; Pred. No. 8e-249;  
Matches 995; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 GTGTCTATGATCCGGGAGAAAGCTGGGCTCGGTCGCTTCTCTGAGGTGATGTGCCCC 60



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QY 382 TAACAGGTGGTGAACCTGTTTGACCGCATCATGGAGCGGGGCTCCTACACAGAGAAGGACG 441
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QY 742 ATGATGAGAGCGATCCTGAACTCTTCAGCCAGATTCTGAGGGCCAGCTATGAGTTGACT 801
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QY 922 ATGCAGCCTTCGATAGGACATCCTGGGTTCTGTAGTGAGCAGATCCAGAGAATTTTG 981
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RESULT 2
LOCUS CR6111192 1525 bp mRNA linear HTC 21-JUL-2004
DEFINITION full-length cDNA clone CS0DI079YD13 of Placenta Cot 25-normalized
of Homo sapiens (human).
ACCESSION CR6111192
VERSION CR6111192.1 GI:50491999
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KEYWORDS HTC; CNSLT_cDNA.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1525)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
REMARK Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue
REFERENCE 2 (bases 1 to 1525)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
COMMENT 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
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Best Local Similarity 75.6%; Pred. No. 7.9e-206;
Matches 1135; Conservative 0; Mismatches 282; Indels 85; Gaps 5;
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QY 195 CTGGCCCCAGGAAAGGGGCTCTGCTCATCTTGTGGCCCTCAAGTGCATTCCTCAAGAAAGCA 254
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QY 255 CTTGGGGCAAGGAGGCCCTTGGTGAGAAATGAGATCGCGGTACTTCGCAGAAATCAGCCAT 314
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QY 435 AAGGACGCCAGCCACCTTGTAGGGCAGGTCTTGGCGCTGTCTCCTACCTTCATAGCCTG 494
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QY 495 GGCATCGTGACCGGGACCTCAAGCCTGAAACCTCCTCTATGCCACACCTTTTGAGGAC 554
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QY 555 TCCAAGATCATGTTCTCTGACTTTTGGCCTGTGCAAAAATACAAGCTGGCAACATGCTAGGC 614
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Db 565 ACCGCCTGTGGGACCCCTGGATATGCCGAGCCAGTGACACTGAGCGGATGGCTGCGTGT 624  
  
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Db 625 GTGCCTGTGCGTGTCTGTCTGTCTGTCTGTGGCCCCCAGCCCCAGAGCTCTTGGAGCAAAA 684  
  
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Db 1514 CC 1515

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DEFINITION AGENCOURT\_11275610 NIH\_MGC\_164 Mus musculus cDNA clone

IMAGE:30144610 5', mRNA sequence.  
CA978376  
VERSION CA978376.1 GI:27511030  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 921)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Dr. David Rowe and Dr. Mina  
cDNA Library Preparation: Invitrogen Corp  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: NDAM0057 row: f column: 11  
High quality sequence stop: 721.  
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FEATURES  
source

ORIGIN

Query Match 53.0%; Score 823.2; DB 6; Length 921;  
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Db 428 GGGACATCCTGGGTTCTGTCTCAGTGAGCAGATCCAGAAGAATTTTGCCAGGACCCACTGGA 487  
QY 997 AGCGTGCAATCAATGCCACATCATCTCTACGTACATCCGTAAAGCTGGGACAAAGCCAG 1056  
Db 488 AGCGTGCAATCAATGCCACATCATCTCTACGTACATCCGTAAAGCTGGGACAAAGCCAG 547  
QY 1057 AGGGTGAGGAGGCCCTCCAGGCAGTGTATGACCCCGTCATAGCCACCCAGGCCCTTGGGACTA 1116  
Db 548 AGGGTGAGGAGGCCCTCCAGGCAGTGTATGACCCCGTCATAGCCACCCAGGCCCTTGGGACTA 607  
QY 1117 GCCAGTCCCCCAAGTGTGAAACCAGGTAGATGCCAAGGAAGGCCAAAGTGACTGACTC 1176  
Db 608 GCCAGTCCCCCAAGTGTGAAACCAGGTAGATGCCAAGGAAGGCCAAAGTGACTGACTC 667  
QY 1177 CCGGTTTTTCTTCTCCAGCCCTTTTGGTCTCTTTCTCTGGATCCTTGTCTCCAGACTG 1236  
Db 668 CCGGTTTTTCTTCTCCAGCCCTTTTGGTCTCTTTCTCTGGATCCTTGTCTCCAGACTG 727  
QY 1237 GCCTCTGTGGAAGCTCGAGACTGGGTGTGATGCATGGCCACTAGGGTACGGGCTTCCC 1296  
Db 728 GCCTCTGTGGAAGCTCGAGACTGGGTGTGATGCATGGCCACTAGGGTACGGGCTTCCC 787  
QY 1297 CAGTATGTCCCCCAGCCCTCTATTCTTACCTATGGTGGAGGCTCCCTTT 1344  
Db 788 CAGTATGTCCCCCAGCCCTCTATTCTTACCTATGGTGGAGGCTCCCTT 835

RESULT 4  
AY418572  
LOCUS AY418572 995 bp DNA linear GSS 12-DEC-2003  
DEFINITION Homo sapiens HCM6602 gene, VIRTUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
ACCESSION AY418572  
VERSION AY418572.1 GI:39774532  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 995)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 995)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT These sequences were made by sequencing genomic exons and ordering  
them based on alignment.  
FEATURES Location/Qualifiers  
source 1..995  
/organism="Homo sapiens"  
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gene <1..>995  
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Query Match 51.9%; Score 806.2; DB 9; Length 995;  
Best Local Similarity 88.1%; Pred. No. 2e-199;  
Matches 877; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

QY 142 GTGTCTATGAGATCCGGGAGAAAGCTGGGCTCGGCTGCCTTCTCTGAGGTGATGCTGGCCC 201  
Db 1 CGGTCTACGAGATCCGCGAGAGGCTCGGCTCGGCTGCCTTCTCCGAGGTGCTGCTGGCCC 60  
QY 202 AGAAAGGGGCTCTGTCTCATCTTGTGGCCCTCAAGTGCATTCCCAAGAAAGCACTTCGGG 261  
Db 61 AGAGCGGGGCTCCGCACACCTCGTGGCCCTCAAGTGCATCCCAAGAAAGSCCTCCGGG 120  
QY 262 GCAAGGAGGCCCTGGTGAGAAATGAGATCGCGGTACTTCGCAGAATCAGCCATCCCAACA 321  
Db 121 GCAAGGAGGCCCTGGTGAGAAACGAGATCGAGTCTCCGTAGGATCAGTACACCCCAACA 180  
QY 322 TTGTGGCTCTGGAGGACGTCCATGAGAGTCTTCTCATCTCTACTTTGGCCATGGAGCTGG 381  
Db 181 TCGTCGCTCTGGAGGATGTCCACGAGAGCCCTTCCACCTCTACCTGGCCATGGAAGTGG 240  
QY 382 TAACAGGTGTGAACCTGTTTGACCCGCATCATGGAGCGGGCTCCTACACAGAGAAGGACG 441  
Db 241 TGACGGGTGGCAGACTGTTTGACCCGCATCATGGAGCGGGCTCCTACACAGAGAAGGATG 300  
QY 442 CCAGCCACCTTGTAGGGCAGGTCCCTTGGCGGTGTCTCCTACCTTCATAGCCTGGGCATCG 501  
Db 301 CCAGCCATCTGGTGGGTGAGTCCCTTGGCGCGTCTCCTACCTGCACAGCCTGGGGATCG 360  
QY 502 TGCACCGGGACCTCAAGCCTGAAACCTCTCTATGCCACACCTTTTGGAGACTCCCAAGA 561  
Db 361 TGCACCGGGACCTCAAGCCCGAAACCTCTGTATGCCACGCCCTTTGAGGACTCGAAGA 420  
QY 562 TCATGGTCTCTGACTTTGGCCCTGTCCAAAATACAAAGCTGGCAACATGCTAGCACAGCCT 621  
Db 421 TCATGGTCTCTGACTTTGGACTCTCCAAAATCCAGGCTGGGAACATGCTAGCACCCGCT 480  
QY 622 GTGGACCCCAAGGATATGTGGCCCAAGAGTCTCTGGAGCAGAAACCTACGGGAAGGCCG 681  
Db 481 GTGGACCCCTGGATATGTGGCCCAAGAGTCTTGGAGCAGAAACCTACGGGAAGGCCG 540  
QY 682 TAGATGTGTGGGCCCTGGGTGTCACTCTCCACAGATCTTGAGGGCCAGCTATGAGTTTGACT 741  
Db 541 TAGATGTGTGGGCCCTGGGCGTCACTCTCTACATCCTGTGTGGGTACCCCTTCT 600  
QY 742 ATGATGAGAGCGATCCTGAACTCTTCAGCCAGATCTTGAGGGCCAGCTATGAGTTTGACT 801  
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QY 802 CCCCCTTTTGGATGACATCTCAGAATCAGCCAAAGACTTCATTCCGCCACCTTCTGGAAC 861  
Db 661 CTCCTTTCTGGGATGACATCTCAGAATCAGCCAAAGACTTCATCCGGCACCTTCTGGAGC 720  
QY 862 GTATCCCCCAGAAAGAGGTTACCTGCCAGCAGGCCCTACAGCATCTTTGGATCTCTGGGG 921  
Db 721 GAGACCCCCAGAAAGAGGTTACCTGCCAACAGGCCCTTGGGCACCTTTGGATCTCTGGGG 780  
QY 922 ATGAGCCTTCGATAGGGACATCCTGGGTTCTGTCTGAGTGAGCAGATCCAGAGAATTTTG 981  
Db 781 ACACAGCCTTCGACAGGGACATCTTAGGCTCTGTCTGAGTGAGCAGATCCGGAAGAACTTG 840  
QY 982 CCAGGACCCCACTGGAAGCGTGCATTCAATGCCACATCATTCCTACGTACATCCGTAAAGC 1041  
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QY 1102 CAGGCCCTTGGGACTAGCCAGTCCCCCAAGTGGTGA 1136  
Db 961 CAGGCCCTCCGTGCTGGCCAGCCCCCAAGTGGTGA 995

RESULT 5  
BU524572  
LOCUS BU524572 742 bp mRNA linear EST 13-SEP-2002



DEFINITION AGENCOURT 10100571 NIH MGC 144 Mus musculus cDNA clone  
IMAGE:6532158 5', mRNA\_sequence.  
ACCESSION BU524572  
VERSION BU524572.1 GI:22835011  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 742)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Dr. Michael Brownstein  
cDNA Library Preparation: Michael Brownstein Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LCM2686 row: k column: 06  
High quality sequence stop: 495.  
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/clone="IMAGE:6532158"  
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/clone\_lib="NIH MGC 144"  
/note="Organ: Brain; Vector: pDNR-LIB; Site 1: SfiI  
(ggccattatggcc); Site 2: SfiI (ggccgcctcgcc); cDNA made  
by oligo-dT priming and directionally cloned. 5' and 3'  
adaptors were used in cloning as follows:  
5'-AAGCAGTGGTATCAAGCAGAGTGGCATTACGGCGGG-3' and  
5'-ATTCTAGAGCCGAGGCGGCACATG-dT(30)NN-3'. Full-length  
enriched library was constructed using the Clontech  
Creator SMART kit and size-selected to contain the 0.2-0.5  
kb size fraction (other fractions present in NIH MGC 143).  
Library created in the laboratory of M. Brownstein (NIH,  
NIH). Note: this is a NIH\_MGC Library."

FEATURES  
source  
Location/Qualifiers  
1..742  
/organism="Mus musculus"  
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/db\_xref="taxon:10090"  
/clone="IMAGE:6532158"  
/lab\_host="DH10B (T1-phage-resistant)"  
/clone\_lib="NIH MGC 144"  
/note="Organ: Brain; Vector: pDNR-LIB; Site 1: SfiI  
(ggccattatggcc); Site 2: SfiI (ggccgcctcgcc); cDNA made  
by oligo-dT priming and directionally cloned. 5' and 3'  
adaptors were used in cloning as follows:  
5'-AAGCAGTGGTATCAAGCAGAGTGGCATTACGGCGGG-3' and  
5'-ATTCTAGAGCCGAGGCGGCACATG-dT(30)NN-3'. Full-length  
enriched library was constructed using the Clontech  
Creator SMART kit and size-selected to contain the 0.2-0.5  
kb size fraction (other fractions present in NIH MGC 143).  
Library created in the laboratory of M. Brownstein (NIH,  
NIH). Note: this is a NIH\_MGC Library."

ORIGIN  
Query Match 44.2%; Score 686.4; DB 5; Length 742;  
Best Local Similarity 99.7%; Pred. No. 4e-168;  
Matches 698; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 186 GAGGTGATGCTGGCCAGGAAAGGGGCTCTGCTCATCTTGTGGCCCTCAAGTGCATTCCC 245  
Db |||||  
3 GAGGTGATGCTGGCCAGGAAAGGGGCTCTGCTCATCTTGTGGCCCTCAAGTGCATTCCC 62

QY 246 AAGAAAGCACTTCGGGGCAAGGAGGCCCTGGTGGAGATGAGATCGCGGTACTTCGCAGA 305  
Db |||||  
63 AAGAAAGCACTTCGGGGCAAGGAGGCCCTGGTGGAGATGAGATCGCGGTACTTCGCAGA 122

QY 306 ATCAGCCATCCCAACATTGTGGCTCTGGAGGACGTTCATGAGATCCTTCTCATCTCTAC 365  
Db |||||  
123 ATCAGCCATCCCAACATTGTGGCTCTGGAGGACGTTCATGAGATCCTTCTCATCTCTAC 182

QY 366 TTGGCCATGGAGCTGGTAAACAGGTGGTGAACACTGTTGACCGCATCATGGAGCGGGCTCC 425  
Db |||||  
183 TTGGCCATGGAGCTGGTAAACAGGTGGTGAACACTGTTGACCGCATCATGGAGCGGGCTCC 242

QY 426 TACACAGAGAAGGACCGCAGCCACCTTGTAGGGCAGGTCTTGGCGTGTCTCTCTACCTT 485  
Db |||||  
243 TACACAGAGAAGGACCGCAGCCACCTTGTAGGGCAGGTCTTGGCGTGTCTCTCTACCTT 302

QY 486 CATAGCCTGGGCATCGTGCACCGGGACCTCAAGCCTGAAACCTCCTCTATGCCACACCT 545  
Db |||||  
303 CATAGCCTGGGCATCGTGCACCGGGACCTCAAGCCTGAAACCTCCTCTATGCCACACCT 362

QY 546 TTTGAGGACTCCAAGATCATGGTCTCTGACTTTGGCCTGTCCAAAATACAAAGCTGGCAAC 605  
Db |||||  
363 TTTGAGGACTCCAAGATCATGGTCTCTGACTTTGGCCTGTCCAAAATACAAAGCTGGCAAC 422

QY 606 ATGCTAGGCACAGCCTGTGGGACCCAGGATATGTGGCCCGCAGAGCTCCTGGAGAGAAA 665  
Db |||||  
423 ATGCTAGGCACAGCCTGTGGGACCCAGGATATGTGGCCCGCAGAGCTCCTGGAGAGAAA 482

QY 666 CCCTACGGGAAGCGCTAGATGTGTGGCCCTGGGTGTCTCTACATCCTGCTGTGT 725  
Db |||||  
483 CCCTACGGGAAGCGCTAGATGTGTGGCCCTGGGTGTCTCTCTACATCCTGCTGTGT 542

QY 726 GGTACCCCTTCTATGATGAGAGCGATCCTGAACTCTTCAGCCAGATTCTGAGGGCC 785  
Db |||||  
543 GGTACCCCTTCTATGATGAGAGCGATCCTGAACTCTTCAGCCAGATTCTGAGGGCC 602

QY 786 AGCTATGAGTTTGACTCCCCCTTTTGGGATGACATCTCAGAATCAGCCAAAGACTTCATT 845  
Db |||||  
603 AGCTATGAGTTTGACTCCCCCTTTTGGGATGACATCTCAGAATCAGCCCAAGACTTCATT 662

QY 846 CGCCACCTTCTGGAACGTGAT-CCCCAGAGAAGGTTTCACC 884  
Db |||||  
663 CGCCACCTTCTGGAACGTGATCCCCCAGAGAAGGTTTCACC 702

RESULT 6  
BF582563  
LOCUS 602094540F1 NCI\_CGAP\_Co24 Mus musculus cDNA clone IMAGE:4208888 5',  
DEFINITION mRNA sequence.  
ACCESSION BF582563  
VERSION BF582563.1 GI:11656275  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 832)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)  
Tissue Procurement: Jeffrey E. Green, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLAM9773 row: p column: 09  
High quality sequence stop: 717.  
Location/Qualifiers  
1..832  
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/clone="IMAGE:4208888"  
/lab\_host="DH10B (T1 phage-resistant)"  
/clone\_lib="NCI\_CGAP\_Co24"  
/note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
Average insert size 1.6 kb. Constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."

ORIGIN  
Query Match 43.9%; Score 682; DB 2; Length 832;  
Best Local Similarity 95.3%; Pred. No. 5.8e-167;  
Matches 768; Conservative 0; Mismatches 30; Indels 8; Gaps 6;

QY 99 GCAGACATGCTGCTCAAGAAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGG 158  
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Db 25 GCAGACATGCTGCTCAAGAAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGG 84

QY 159 GAGAAGCTGGGCTCGGTCCTTCTCTGAGGTGATGCTGGCCCAAGAAAGGGCTCTGCT 218

Db 85 GAGAAGCTGGGCTCGGTCCTTCTCTGAGGTGATGCTGGCCCAAGAAAGGGCTCTGCT 144

QY 219 CATCTTGTGGCCCTCAAGTGCATTTCCCAAGAAAGCACTTCGGGGCAAGAGCCCTG-GT 277

Db 145 CATCTTGTGGCCCTCAAGTGCATTTCCCAAGAAAGCACTTCGGGGCAAGAGCCCTGTGT 204

QY 278 GGAGAATGAGATCGGGTACTTCGCAGAAATCAGCCATCCCAACATTTGTGGCTCTGGAGGA 337

Db 205 GGAGAATGAGATCGGGTACTTCGCAGAAATCAGCCATCCCAACATTTGTGGCTCTGGAGGA 264

QY 338 CGTCCATGAGAGTCCTTCTCATCTCTACTTTGGCCATGGAGCTGGTAACAGGTGGTGAAC 397

Db 265 CGTCCATGAGAGTCCTTCTCATCTCTACTTTGGCCATGGAGCTGGTAACAGGTGGTGAAC 324

QY 398 GTTTGACCGCATCATGGACGGGGCTCCTACACAGAGAAGGACGCCACCTTGTAGG 457

Db 325 GTTTGACCGCATCATGGACGGGGCTCCTACACAGAGAAGGACGCCACCTTGTAGG 384

QY 458 GCAGGTCTTGGCGCTGTCTCCTACCTTTCATAGCCTGGGCATCGTGCACCGGACCTCAA 517

Db 385 GCAGGTCTTGGCGCTGTCTCCTACCTTTCATAGCCTGGGCATCGTGCACCGGACCTCAA 444

QY 518 GCCTGAAAACCTCCTCTATGCCCACACCTTTTGGAGACTCCAAGATCATGGTCTCTGACTT 577

Db 445 GCCTGAAAACCTCCTCTATGCCCACACCTTTTGGAGACTCCAAGATCATGGTCTCTGACTT 504

QY 578 TGGCCTGTCCAAAATACAAGCTGGCAACATGCTAGGCACAGCCTGTGGGACCCAGGATA 637

Db 505 TGGCCTGTCCAAAATACAAGCTGGCAACATGCTAGGCACAGCCTGTGGGACCCAGGATA 564

QY 638 TGTGGCCCCAGAGCTCCTTGAGCAGAAACCCCTACGGGAAGGCCGT-AGATGTGTGGGCC 696

Db 565 TGTGGCCCCAGAGCTCCTTGAGCAGAAACCCCTACGGGAAGGCCGTGAGATGTGTGGGCC 624

QY 697 TGGGTGTCTATCTCCTACATGCTGCTGTG-TGGGTACCCCCCTTCTATGATGAGAGCCGAT 755

Db 625 TGGGTGTCTATCTCCTACATGCTGCTGTGTTGGGTACCCCCCTTCTATGATGAGAGCCGA 684

QY 756 CTTGAAC--TCTTCAGCCAGATTCTGAGGGCCAGCTATGAGTTTGACT--CCCCCTTTG 811

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QY 812 GGATGACATCTCAGA-ATCAGCCAAAGACTTTCATTGCGCACCTTCTTGGAACTGATCCCC 870

Db 745 GGATGACCTCTCTCAGAAATCAGCAAAGAAATTTCATTGCGCACCTTCTTGGAAAGTGAATCCC 804

QY 871 AGAAGAGTTTACCTGCCAGCAGGCC 896

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RESULT 7  
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DEFINITION Pan troglodytes HCM6602 gene, VIRTUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.  
ACCESSION AY418573  
VERSION AY418573.1 GI:39774533  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
AUTHORS 1 (bases 1 to 964)  
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous

JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 964)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT These sequences were made by sequencing genomic exons and ordering  
them based on alignment.  
FEATURES  
Location/Qualifiers  
source 1..964  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
<1..>964  
/locus\_tag="HCM6602"  
gene  
ORIGIN

Query Match 43.4%; Score 675; DB 9; Length 964;  
Best Local Similarity 76.6%; Pred. No. 4.1e-165;  
Matches 738; Conservative 0; Mismatches 226; Indels 0; Gaps 0;

QY 173 GGGTGCCTTCTCTGAGGTGATGCTGGCCAGGAAAGGGCTCTGCTCATCTGTGGCCCT 232

Db 1 GGGTGCCTNNNCCGAGGTGGTGTGGCCAGGAGCGGGGCTCCGCACACCTCGTGGCCCT 60

QY 233 CAAGTGCATTTCCCAAGAAAGCACTTCGGGGCAAGGAGGCCCTGGTGGAGAAATGAGATCGC 292

Db 61 CAAGTGCATTTCCCAAGAAAGGCCCTCCGGGGCAAGGAGGCCCTGGTGGAGAACGAGATCGC 120

QY 293 GGTACTTCGCAGAAATCAGCCATCCCCAACATTTGTGGCTCTTGAGGACGTCCTCAGAGATCC 352

Db 121 AGTGCTCCGTAGGATCAGTCACCCCAACATCGTCGCTCTGGAGGATGTCCACGAGAGCCC 180

QY 353 TTCTCATCTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAACCTGTTTGACCGCATCAT 412

Db 181 TTCCCACCTCTACTGGCCATGGAACCTGGTGACGGGNGCGAGCTGTTTGACCGCATCAT 240

QY 413 GGAGCGGGGCTCCTACACAGAGAAGGACGCCAGCCACCTTGTAGGGCAGGTCCTTGGCGC 472

Db 241 GGAGCGGGGCTCCTACACAGAGAAGGATGCCAGCCANNNGTGGGTGAGTCTTGGCGC 300

QY 473 TGTCTCCTACCTTCATAGCCTGGGCATCGTGACCGGACCTCAAGCCTGAAAACTCCT 532

Db 301 CGTCTCCTACCTGCACAGCCTGGGATCGTGACCGGACCTCAAGCCCCGAAAACTCCT 360

QY 533 CTATGCCACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTGGCCTGTCCAAAAAT 592

Db 361 GTATGCCACCGCCTTTGAGGACTCGAAGATCATGGTCTCTGACTTTGGACTCTCCAAAAAT 420

QY 593 ACAAGCTGGCAACATGCTAGGCACAGCCCTGTGGGACCCCAAGGATATGTGGCCCAAGAGCT 652

Db 421 CCAGGTGGGAACATGCTAGGCACCGCCTGTGGACCCCTGGATATGTGGCCCAAGAGCT 480

QY 653 CCTGGAGCAGAAACCTTACGGGAAGCCCGTAGATGTGTGGCCCTGGGTGTCTCTCCTA 712

Db 481 CTTGGAGCAGAAACCTTACGGGAAGCCCGTAGATGTGTGGCCCTGGGCGTCTCTCCTA 540

QY 713 CATCCTGTGTGGGTACCCCCCTTCTATGATGAGAGCGATCCTGAACCTCTTCAGCCA 772

Db 541 CATCCTNN 600

QY 773 GATTCTGAGGGCCAGCTATGAGTTTGACTCCCCCTTTTGGGATGACATCTCAGAATCAGC 832

Db 601 NNN 660

QY 833 CAAAGACTTTCATTGCGCACCTTCTTGGAACGTGATCCCCAGAGAGGTTTACCTGCCAGCA 892

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QY	893	GGCCTACAGCATCTTTGGATCTCTGGGATGTCAGCCTTCGATAGGACATCCTGGGTC	952
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QY	953	TGTCAGTGAGCAGATCCAGAAGAAATTTGCCAGGACCCACTGGAAGCGTGCAATCAATGC	1012
Db	781	TGTCAGTGAGCAGATCCGGAAGAACTTTGCTCGGACACACTGGAAGCGACCTTCAATGC	840
QY	1013	CACATCAATTCCTACGTACATCCGTAAGCTGGGACAAAGCCCAGAGGGTGAGGAGCCCTC	1072
Db	841	CACCTGTTCTCTGGCCACATCCGGAAGCTGGGCGAGATCCAGAGGGCGAGGGGCCCTC	900
QY	1073	CAGGCAGTGATGACCCGTACATAGCCACCCAGGCGCTTGGACTAGCCAGTCCCCCAAGTG	1132
Db	901	TCAGCAGGGCATGGCCCCGCCACAGCCACTCAGGCGCTCCATGCTGGCCAGCCCCCAAGTG	960
QY	1133	GTGA	1136
Db	961	GTGA	964
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DEFINITION	AGENCOURT 11214785 NIH_MGC_135 Mus musculus cDNA clone		
	IMAGE:30133689 5', mRNA sequence.		
ACCESSION	CB192924		
VERSION	CB192924.1 GI:28215131		
KEYWORDS	EST.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
TITLE	1 (bases 1 to 932)		
JOURNAL	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgapbs-r@mail.nih.gov">cgapbs-r@mail.nih.gov</a> Tissue Procurement: Dr. David Rowe cDNA Library Preparation: Invitrogen Corp cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: NDAM0028 row: 0 column: 10 High quality sequence stop: 574.		
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	/clone="IMAGE:30133689"		
	/lab_host="DH10B (phage-resistant)"		
	/clone_lib="NIH MGC 135"		
	/note="Vector: pCMVSPORT6.1; Site 1: EcoRV; Site 2: NotI; Normalized full-length enriched library from pooled mouse embryonic limb, maxilla and mandible, day 12.5, 13.5, 14.5, and 15.5 (size selected for the 0.5-1 kb fragments) Cloned directionally, priming method: Oligo-dT. cDNA enrichment: >1k bp, Average insert size 1.6k bp. Normalization (Cot value): 7.5 kb. Priming sequence: 5'GACTAGTTCTAGATCGGAGCGGCCGCC(T)3' Tissue contributed by, David Rowe. Library constructed by ResGen, Invitrogen Corp."		
ORIGIN			
Query Match	42.1%;	Score 654.2;	DB 6; Length 932;
Best Local Similarity	96.3%;	Pred. No. 1.1e-159;	
Matches 702; Conservative	0;	Mismatches 23;	Indels 4; Gaps 3;

QY	712	ACATCTGTGTGGGTACCCCCCTTCTATGATGAGAGCGATCCTGAACCTCTCAGCC	771
Db	1	ACATCTGTGTGGGTACCCCCCTTCTATGATGAGAGCGATCCTGAACCTCTCAGCC	60
QY	772	AGATTCTGAGGGCCAGCTATGAGTTTGACTCCCTTTGGGATGACATCTCAGAATCAG	831
Db	61	AGATTCTGAGGGCCAGCTATGAGTTTGACTCCCTTTGGGATGACATCTCAGAATCAG	120
QY	832	CCAAAGACTTCATTGCGCACCTTCTGGAACGTGATCCCCAGAAAGAGGTTTCACTGCCAGC	891
Db	121	CCAAAGACTTCATTGCGCACCTTCTGGAACGTGATCCCCAGAAAGAGGTTTCACTGCCAGC	180
QY	892	AGGCCCTACAGCATCTTTGGATCTCTGGGGATGCAGCCTTCGATAGGGACATCCTGGGTT	951
Db	181	AGGCCCTACAGCATCTTTGGATCTCTGGGGATGCAGCCTTCGATAGGGACATCCTGGGTT	240
QY	952	CTGTCACTGAGCAGATCCAGAAGAATTTTCCAGGACCCACTGGAAGCGTGCAATCAATG	1011
Db	241	CTGTCACTGAGCAGATCCAGAAGAATTTTCCAGGACCCACTGGAAGCGTGCAATCAATG	300
QY	1012	CCACATCATTCCTACGTACATCCGTAAGCTGGGACAAAGCCCAGAGGGTGAGAGGCCT	1071
Db	301	CCACATCATTCCTACGTACATCCGTAAGCTGGGACAAAGCCCAGAGGGTGAGAGGCCT	360
QY	1072	CCAGGCAGTGATGACCCGTATAGCCACCCAGCCCTTTGGGACTAGCCAGTCCCCCAAGT	1131
Db	361	CCAGGCAGTGATGACCCGTATAGCCACCCAGCCCTTTGGGACTAGCCAGTCCCCCAAGT	420
QY	1132	GGTGAACACCAGGTAGATGCCAAGGAAGGCCAAGTGGACTGACTCCCGGTTTCTTTCC	1191
Db	421	GGTGAACACCAGGTAGATGCCAAGGAAGGCCAAGTGGACTGACTCCCGGTTTCTTTCC	480
QY	1192	TCCAGCCCTTTTGGTCTCTTTCTCTGGATCCTTGCTCCAGACTGGCCCTCTGCTGAAAG	1251
Db	481	TCCAGCCCTTTTGGTCTCTTTCTCTGGATCCTTGCTCCAGACTGGCCCTCTGCTGAAAG	540
QY	1252	TCTGAGACTGGGTGTGATGCATGGCACTAGGGTACGGGGCTTCCCCAGTATGTCCCCCAG	1311
Db	541	TCTGAGACTGGGTGTGATGCATGGCACTAGGGGACGGGGCTTCCCCAGTATGTCCCCCAG	600
QY	1312	CC-TCTATTCTTACCTATGGTGGAGGCTCCCTTCCCATGTGCTGCCACCTCTAT-GG	1369
Db	601	CCTTCGATTCTTACCCTTGGTGAAGCTCCCGTTTCCATGGCGCTGCCACGCTCTATGGG	660
QY	1370	AAACTGAGGAGGTGTTCAAAAGTGGACTTGGGAGCCAT--CCTTCCTGCACCTTGACCA	1427
Db	661	AAACCGACGAAGTGTCAAAAGTGGACTTGGGAAGCATCACTTCCTGGCACCTTGGGAAGA	720
QY	1428	ACACATGCA	1436
Db	721	AAACAAGGA	729
RESULT 9			
AU079915			
LOCUS	AU079915	787 bp	mRNA linear EST 12-JUL-2000
DEFINITION	AU079915 Sugano mouse brain mncb Mus musculus cDNA clone MNCb-4938		
	5', mRNA sequence.		
ACCESSION	AU079915		
VERSION	AU079915.1 GI:6084670		
KEYWORDS	EST.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
TITLE	1 (bases 1 to 787)		
JOURNAL	Hashimoto, K., Kusuda, J., Tanuma, R., Ito, A., Hirata, M., Toyoda, A., Suzuki, Y., Sasaki, M. and Sugano, S.		
COMMENT	Isolation of full-length cDNA clones from a mouse brain cDNA library made by oligo-capping method Unpublished (1999) Contact: Katsuyuki Hashimoto Division of Genetic Resources		





QY 278 GGAGATGAGATCGCGGTACTTCGCAGAAATCAGCCATCCCAACATTGTGGCTCTGGAGGA 337  
Db 302 GGAGATGAGATCGCGGTACTTCGCAGAAATCAGCCATCCCAACATTGTGGCTCTGGAGGA 361  
QY 338 CGTCCATGAGATCCTTCTCATCTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAAC 397  
Db 362 CGTCCATGAGATCCTTCTCATCTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAAC 421  
QY 398 GTTGACCGCATCATGGAGCGGGCTCCTACACAGAGAAGGACGCCACCTTGTAGG 457  
Db 422 GTTGACCGCATCATGGAGCGGGCTCCTACACAGAGAAGGACGCCACCTTGTAGG 481  
QY 458 GCAGGTCTTGGCGCTGTCTCTACCTTACATAGCCTGGGCATCGTGACCGGGACCTCAA 517  
Db 482 GCAGGTCTTGGCGCTGTCTCTACCTTACATAGCCTGGGCATCGTGACCGGGACCTCAA 541  
QY 518 GCCTGAAAACCTCCTCTATGCCACACACCTTTTGGAGACTCCAAAGATCATGGTCTCTGACTT 577  
Db 542 GCCTGAAAACCTCCTCTATGCCACACACCTTTTGGAGACTCCAAAGATCATGGTCTCTGACTT 601  
QY 578 TGSCTGTCCAAAATACAAGCTGGCAACATGCTAGGCACAGCCTGTGGGACCCAGGATA 637  
Db 602 TGGCTGTCCAAAATACAAGCTGGCAACATGCTAGGCACAGCCTGTGGGACCCAGGATA 661  
QY 638 TGTGGCCCCAGAGCTCCTGGAGCAGAAACCCCTACGGGAAGGCCGTAGATGTGTGGCCCT 697  
Db 662 TGTGGCCCCAGAACTCCTGGAGCANAAACCCCTACNGGAAGGCCGTANATGTGTGGCCCT 721  
QY 698 GGTGTCTATCTCTACATCCTGTGTGGGTACCCCCCTTCTAT 743  
Db 722 GGTGTCTATCTNCTACATNCTGTGGTGGGTACCCCCCTTCTAT 767

RESULT 11  
CD776443/c  
LOCUS CD776443 695 bp mRNA linear EST 02-JUL-2003  
DEFINITION UI-M-AQ0-cjc-i-13-0-UI.s1 NIH BMAP\_MHI Mus musculus cDNA clone  
UI-M-AQ0-cjc-i-13-0-UI 3', mRNA sequence.  
ACCESSION CD776443  
VERSION CD776443.1 GI:32434945  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 695)  
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.  
TITLE Normalization and subtraction: two approaches to facilitate gene discovery  
JOURNAL Genome Res. 6 (9), 791-806 (1996)  
MEDLINE 97044477  
PUBMED 8889548  
COMMENT Contact: Chin, H  
National Institute of Mental Health  
6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD  
20892-9643, USA  
Tel: 301 443 1706  
Fax: 301 443 9890  
Email: mEST@mail.nih.gov  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).  
Seq primer: M13 FORWARD  
POLYA=Yes.  
FEATURES  
source Location/Qualifiers  
1..695  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"

/clone="UI-M-AQ0-cjc-i-13-0-UI"  
/dev\_stage="27-32 days"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="NIH\_BMAP\_MHI"  
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified  
polylinker; Site\_1: Not I; Site\_2: Eco RI; The  
NIH BMAP MHI library is a non-normalized library  
constructed from mouse hippocampus. The tag is a string  
of 5 nucleotides present between the Not I site and the  
oligo-dT track. The library was constructed as described  
by Bonaldo, Lennon and Soares, Genome Research 6:  
791-806, 1996. Tissue provided by Ms. Annie Novakovich,  
Zivic-Miller Laboratories.  
TAG TISSUE=hippocampus  
TAG\_LIB=UI-M-AQ0  
TAG\_SEQ=TTCGA"

ORIGIN

Query Match 40.8%; Score 633.8; DB 6; Length 695;  
Best Local Similarity 98.9%; Pred. No. 2.3e-154;  
Matches 690; Conservative 0; Mismatches 3; Indels 5; Gaps 5;  
QY 857 GGAACGTGATCCCGAAGAGGTTTCACCTGCCAGAGGCCCTACAGCATCTTTGGATCTC 916  
Db 695 GGAACGTGATCCCGAAGGA-GTTCACTGCCAGAGGCCCTACAGCATCTNT-GATCTC 638  
QY 917 TGGGGATGCAGCCTTCGATAGGGACATCCTGGGTCTGTCAAGTGCAGATCCAGAAGAA 976  
Db 637 TGGGGAT-CAGCCTTCGATAGGGACATCCTGGG-TCTGTCAAGTGCAGATCCAGAAGAA 580  
QY 977 TTTTGCCAGGACCCACTGGAAGCGTGCAATTCATGCCACATCATTCCTACGTCAATCCG 1036  
Db 579 -TTTGCCAGGACCCACTGGAAGCGTGCAATTCATGCCACATCATTCCTACGTCAATCCG 521  
QY 1037 TAAGCTGGGACAAAGCCCAGAGGGTGAGGAGGCCCTCCAGGCAGTGATGACCCGTCATAG 1096  
Db 520 TAAGCTGGGACAAAGCCCAGAGGGTGAGGAGGCCCTCCAGGCAGTGATGACCCGTCATAG 461  
QY 1097 CCACCCAGGCCCTTGGACTAGCCAGTCCCCCAAGTGGTGAAACCAGGTAGATGCCAAGG 1156  
Db 460 CCACCCAGGCCCTTGGACTAGCCAGTCCCCCAAGTGGTGAAACCAGGTAGATGCCAAGG 401  
QY 1157 AAGGCCAAGTGGACTGACTCCCGGTTTTTCTTCTCCAGCCCTTTTGGTCTCTTCCTG 1216  
Db 400 AAGGCCAAGTGGACTGACTCCCGGTTTTTCTTCTCCAGCCCTTTTGGTCTCTTCCTG 341  
QY 1217 GATCCTTGTCTCCTCCAGACTGGCCTCTGCTGGAAAGTCTGAGACTGGGTGTGATGATGGC 1276  
Db 340 GATCCTTGTCTCCTCCAGACTGGCCTCTGCTGGAAAGTCTGAGACTGGGTGTGATGATGGC 281  
QY 1277 ACTAGGGTACGGGGCTTCCCCAGTATGTCCCCCAGCCTCTATTCTTACCTATGGTGAGG 1336  
Db 280 ACTAGGGTACGGGGCTTCCCCAGTATGTCCCCCAGCCTCTATTCTTACCTATGGTGAGG 221  
QY 1337 CTCCCTTTCCCATGTGCTGCCACCCTCTATGGAAGTGGAGGTGTTCAAAAGTGGAC 1396  
Db 220 CTCCCTTTCCCATGTGCTGCCACCCTCTATGGAAGTGGAGGTGTTCAAAAGTGGAC 161  
QY 1397 TTGGGAGCCATCCTTCTCTGCACCTTGCACGAACACATGTCATTTGTGGCTGTTCTGTGCT 1456  
Db 160 TTGGGAGCCATCCTTCTCTGCACCTTGCACGAACACATGTCATTTGTGGCTGTTCTGTGCT 101  
QY 1457 TTGCTGACTGTGGGTGGTCTGCTTGTGTGTGGGCCCTTTAGTTCCCTCTTCCCTAACCC 1516  
Db 100 TTGCTGACTGTGGGTGGTCTGCTTGTGTGTGGGCCCTTTAGTTCCCTCTTCCCTAACCC 41  
QY 1517 AATAAGACAAACAGAACCAAAAAAATAAAAAA 1554  
Db 40 AATAAGACAAACAGAACCAAAAAAATAAAAAA 3

RESULT 12  
BG695422









GenCore version 5.1.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: June 6, 2005, 05:55:06 ; Search time 233 Seconds  
(without alignments)  
6830.653 Million cell updates/sec

Title: US-10-032-254A-1  
Perfect score: 2872  
Sequence: 1 gttcgaggagtcctccactc.....caaaaaaaaaaaaaaaaaaa 1554

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1612378 seqs, 512079187 residues 3224756

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-Q=/cgn2\_1/USFTO\_spool\_p/US10032254/runat\_02062005\_131019\_3593/app\_query.fasta\_1.1735  
-DB=UniProt\_03 -QFMT=fastan -SUFFIX=rup -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100 -THR\_MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10032254 @CGN 1 1 159 @runat\_02062005\_131019\_3593 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV\_TIMEOUT=120 -WARN\_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : UniProt\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1801	62.7	355	2 Q80W07	Q80w07 mus musculus
2	1787	62.2	343	2 Q9QYK9	Q9qyk9 mus musculus
3	1769	61.6	343	2 O70150	O70150 rattus norv
4	1682.5	58.6	342	2 O08767	O08767 rattus norv
5	1377.5	48.0	337	2 Q7T2H4	Q7t2h4 xenopus lae
6	1208	42.1	241	2 Q6P2M8	Q6p2m8 homo sapien
7	1205.5	42.0	378	2 Q8AVN4	Q8avn4 xenopus lae
8	1200.5	41.8	382	2 Q8AYR2	Q8ayr2 xenopus lae
9	1192.5	41.5	395	2 Q6GM90	Q6gm90 xenopus lae
10	1188.5	41.4	374	1 KCC1_MOUSE	Q91ys8 mus musculus
11	1188.5	41.4	374	1 KCC1_RAT	Q63450 rattus norv
12	1184.5	41.2	370	1 KCC1_HUMAN	Q14012 homo sapien
13	1184.5	41.2	395	2 Q8AYR3	Q8ayr3 xenopus lae
14	1173.5	40.9	357	2 Q9HD31	Q9hd31 homo sapien
15	1173.5	40.9	385	2 Q8IU85	Q8iu85 homo sapien
16	1171.5	40.8	385	2 Q8BW96	Q8bw96 mus musculus

17	1148.5	40.0	367	2 Q8BWI7	Q8bwi7 mus musculu
18	1148.5	40.0	388	2 Q64HW3	Q64hw3 oncorhynchu
19	1122.5	39.1	377	2 Q80W64	Q80w64 mus musculu
20	1105.5	38.5	299	2 Q8BJA6	Q8bja6 mus musculu
21	1073	37.4	477	2 Q91VB2	Q91vb2 mus musculu
22	1072	37.3	476	2 Q7TNJ7	Q7tnj7 rattus norv
23	1065	37.1	460	2 Q86UH5	Q86uh5 homo sapien
24	1065	37.1	481	2 Q9Y3J7	Q9y3j7 homo sapien
25	1063	37.0	476	2 Q96NX5	Q96nx5 homo sapien
26	1055.5	36.8	324	2 Q86SC3	Q86sc3 ciona intes
27	1047	36.5	426	2 Q6PC33	Q6pc33 brachydanio
28	1043.5	36.3	433	2 Q6P965	Q6p965 brachydanio
29	1028.5	35.8	309	2 O08763	O08763 rattus norv
30	1021.5	35.6	408	2 Q7QI42	Q7qi42 anopheles g
31	1016	35.4	377	2 Q7TNJ6	Q7tnj6 rattus norv
32	1015.5	35.4	405	2 Q9V3I4	Q9v3i4 drosophila
33	1014.5	35.3	332	2 Q6V5R5	Q6v5r5 caenorhabdi
34	1014.5	35.3	348	2 Q9TXJ0	Q9txj0 caenorhabdi
35	1010.5	35.2	348	2 Q9UAH6	Q9uah6 caenorhabdi
36	843	29.4	284	2 Q8IGW6	Q8igw6 drosophila
37	839	29.2	284	2 Q8IMB6	Q8imb6 drosophila
38	743	25.9	436	2 Q7SY49	Q7sy49 brachydanio
39	734	25.6	385	2 Q98TZ2	Q98tz2 xenopus lae
40	730	25.4	473	1 KCC4_HUMAN	Q16566 homo sapien
41	728.5	25.4	436	2 Q6STH4	Q6sth4 brachydanio
42	727	25.3	512	2 Q8VD20	Q8vd20 mus musculu
43	726	25.3	377	2 Q6GLS4	Q6gl84 xenopus lae
44	725	25.2	501	2 Q8WTT8	Q8wtt8 homo sapien
45	725	25.2	501	2 Q9BQC9	Q9bqc9 homo sapien

ALIGNMENTS

RESULT 1  
Q80W07  
ID Q80W07 PRELIMINARY; PRT; 355 AA.  
AC Q80W07;  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Pnck protein (Fragment).  
GN Name=Pnck;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Brain;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6; TISSUE=Brain;



RA Strausberg R.;

RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.

CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.

DR EMBL; BC051996; AAH51996.1; -.

DR HSSP; Q63450; 1A06.

DR MGD; MGI:1347357; Pnck.

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.

DR GO; GO:0016740; F:transferase activity; IEA.

DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.

DR InterPro; IPR011009; Kinase like.

DR InterPro; IPR000719; Prot\_kinase.

DR InterPro; IPR002290; Ser\_thr\_kinase.

DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.

DR Pfam; PF00069; Pkinase; 1.

DR ProDom; PD000001; Prot\_kinase; 1.

DR SMART; SM00220; S\_TKc; 1.

DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.

DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.

DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.

KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.

FT NON\_TER 1

SQ SEQUENCE 355 AA; 39444 MW; 5B20F5347F9CC184 CRC64;

Alignment Scores:

Pred. No.:	2.72e-117	Length:	355
Score:	1801.00	Matches:	346
Percent Similarity:	99.14%	Conservative:	1
Best Local Similarity:	98.86%	Mismatches:	3
Query Match:	62.71%	Indels:	0
DB:	2	Gaps:	0

US-10-032-254A-1 (1-1554) x Q80W07 (1-355)

QY 84 GCTGCAAGCAGGGTCGCGACATGCTGCTGCTCAAGAAACAGACGGAGGACATCAGCAGT 143

Db 6 AlaValAlaAlaAlaAspMetLeuLeuLeuLysGlnThrGluAspIleSerSer 25

QY 144 GTCTATGAGATCCGGGAGAGCTGGGCTCGGCTGCTCTCTGAGGTGATGCTGGCCCCAG 203

Db 26 ValTyrGluIleArgGluLysLeuGlySerGlyAlaPheSerGluValMetLeuAlaGln 45

QY 204 GAAAGGGGCTCTGCTCATCTGTGTGGCCCTCAAGTGCAATCCCCAAGAAAGCACTTCGGGGC 263

Db 46 GluArgGlySerAlaHisLeuValAlaLeuLysCysIleProLysLysAlaLeuArgGly 65

QY 264 AAGGAGGCCCTGGTGAGAAATGAGATCGGGTACTTCGAGAATCAGCCATCCCAACATT 323

Db 66 LysGluAlaLeuValGluAsnGluIleAlaValLeuArgArgIleSerHisProAsnIle 85

QY 324 GTGGCTCTGGAGGACGTCCATGAGAGTCCTTCTCATCTCTACTTGGCCATGGAGCTGGTA 383

Db 86 ValAlaLeuGluAspValHisGluSerProSerHisLeuTyrLeuAlaMetGluLeuVal 105

QY 384 ACAGGTGGTGAACCTGTTTGACCGCATCATGGAGCGGGGCTCCTACACAGAGAAGACGCC 443

Db 106 ThrGlyGlyGluLeuPheAspArgIleMetGluArgGlySerTyrThrGluLysAspAla 125

QY 444 AGCCACCTTGTAGGGCAGGTCCTTGGCGCTGTCTCTACCTTCATAGCCTGGGCATCGTG 503

Db 126 SerHisLeuValGlyGlnValLeuGlyAlaValSerTyrLeuHisSerLeuGlyIleVal 145

QY 504 CACCGGGACCTCAAGCCTGAAAACCTCCTCTATGCCACACCTTTTGAGGACTCCAAGATC 563

Db 146 HisArgAspLeuLysProGluAsnLeuLeuTyrAlaThrProPheGluAspSerLysIle 165

QY 564 ATGGTCTCTGACTTTGGCCCTGCCAAAATACAAGCTGGCAACATGCTAGGCACAGCCTGT 623

Db 166 MetValSerAspPheGlyLeuSerLysIleGlnAlaGlyAsnMetLeuGlyThrAlaCys 185

QY 624 GGGACCCCAGGATATGTGGCCCCCAGAGCTCCTGGAGCAGAAACCTACGGGAAGGCCGTA 683

Db 186 GlyThrProGlyTyrValAlaProGluLeuLeuGluGlnLysProTyrGlyLysAlaVal 205

QY 684 GATGTGTGGGCCCTGGGTGTGTCATCTCTACATCCTGTGCTGTGGGTACCCCCCTTCTAT 743

Db 206 AspValTrpAlaLeuGlyValIleSerTyrIleLeuLeuCysGlyTyrProProPheTyr 225

QY 744 GATGAGAGCGATCCTGAACCTCTTCAGCCAGATTTCTGAGGGCCAGCTATGAGTTTGACTCC 803

Db 226 AspGluSerAspProGluLeuPheSerGlnIleLeuArgAlaSerTyrGluPheAspSer 245

QY 804 CCCTTTTGGATGACATCTCAGAATCAGCAAAAGACTTCATTCCGCCACCTTCTTGAACGT 863

Db 246 PropheTrpAspAspIleSerGluSerAlaLysAspPheIleArgHisLeuLeuGluArg 265

QY 864 GATCCCCAGAAGAGGTTTCACCTGCCAGCAGGCCCTACAGCATCTTTGGATCTCTGGGGAT 923

Db 266 AspProGlnLysArgPheThrCysGlnGlnAlaLeuGlnHisLeuTrpIleSerGlyAsp 285

QY 924 GCAGCCTTCGATAGGGACATCCTGGGTTCTGTCTCAGTGAGCAGATCCAGAGAATTTTGCC 983

Db 286 AlaAlaPheAspArgAspIleLeuGlySerValSerGluGlnIleGlnLysAsnPheAla 305

QY 984 AGGACCCACTGGAAGCGTGCATTCAATGCCACATCATTCCTACGTACATCCGTAAGCTG 1043

Db 306 ArgThrHisTrpLysArgAlaPheAsnAlaThrSerPheLeuArgHisIleArgLysLeu 325

QY 1044 GGACAAAGCCCGAGAGGTGAGGAGGCCCTCCAGGCAGTGATGACCCGTCATAGCCACCCA 1103

Db 326 GlyGlnSerProGluGlyGluAlaSerArgGlnCysMetThrArgHisSerHisPro 345

QY 1104 GGCCTTGGGACTAGCCAGTCCCCCAAGTGG 1133

Db 346 GlyLeuGlyThrSerGlnSerProLysTrp 355

RESULT 2

Q9QYK9

ID Q9QYK9 PRELIMINARY; PRT; 343 AA.

AC Q9QYK9;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

DE MCaMK1-beta2 protein (pregnancy upregulated non-ubiquitously expressed

DE CaM kinase) (Pregnancy upregulated nonubiquitous Ca2+/calmodulin-

DE dependent kinase Pnck).

GN Name=Pnck; Synonyms=mCaMK1-beta2;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]\_

RP SEQUENCE FROM N.A.

RA Ueda T., Minami Y.;

RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=FVB/N; TISSUE=Colon;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=FVB/N; TISSUE=Colon;  
RA Strausberg R.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=20139438; PubMed=10673339; DOI=10.1006/geno.1999.6091;  
RA Gardner H.P., Rajan J.V., Ha S.I., Copeland N.G., Gilbert D.J.,  
RA Jenkins N.A., Marquis S.T., Chodosh L.A.;  
RT "Cloning, Characterization, and Chromosomal Localization of Pnck, a  
RT Ca2+/Calmodulin-Dependent Protein Kinase.";  
RL Genomics 63:279-288 (2000).  
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
DR EMBL; AB023027; BAA87926.1; -.  
DR EMBL; BC055891; AAH55891.1; -.  
DR EMBL; AF181984; AAF29157.1; -.  
DR HSSP; Q63450; 1A06.  
DR MGD; MGI:1347357; Pnck..  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR011009; Kinase like.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR002290; Ser\_thr\_kinase.  
DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
DR Pfam; PF00069; Pkinase; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00220; S\_TKc; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 343 AA; 38519 MW; 1B4A28D36E7A936E CRC64;  
  
Alignment Scores:  
Pred. No.: 2.57e-116 Length: 343  
Score: 1787.00 Matches: 343  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 62.22% Indels: 0  
DB: 2 Gaps: 0  
  
US-10-032-254A-1 (1-1554) x Q9QYK9 (1-343)  
  
QY 105 ATGCTGCTCAAGAAACAGACGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAAG 164  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
1 MetLeuLeuLeuLysLysGlnThrGluAspIleSerSerValTyrGluIleArgGluLys 20  
  
QY 165 CTGGCTCGGGTGCCCTTCTGAGGTGATGCTGGCCCAAGGGGCTCTGCTCATCTT 224  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
21 LeuGlySerGlyAlaPheSerGluValMetLeuAlaGlnGluArgGlySerAlaHisLeu 40  
  
QY 225 GTGGCCTCAAGTGCATTCCTCCAGAAAGCACCTTCGGGGCAAGAGGCCCTGGTGGAGAAT 284  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
41 ValAlaLeuLysCysIleProLysLysAlaLeuArgGlyLysGluAlaLeuValGluAsn 60  
  
QY 285 GAGATCGGGTACTTCGCAGAAATCAGCCATCCCAACATTGTGGCTCTGGAGGACGTCAT 344  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
61 GluIleAlaValLeuArgArgIleSerHisProAsnIleValAlaLeuGluAspValHis 80  
  
QY 345 GAGAGTCCTTCTCATCTCTACTTGGCCATGGAGCTGGTAAACAGGTGGTGAACACTGTTGAC 404  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
81 GluSerProSerHisLeuTyrLeuAlaMetGluLeuValThrGlyGlyGluLeuPheAsp 100  
  
QY 405 CGCATCATGGAGCGGGCTCTTACACAGAGAAGGACGCCAGCCACTTGTAGGGCAGGTC 464  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
101 ArgIleMetGluArgGlySerTyrThrGluLysAspAlaSerHisLeuValGlyGlnVal. 120

QY 465 CTTGGCGCTGTCTCCTACCTTCATAGCCTGGGCATCGTGACCGGACCTCAAGCCTGAA 524  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
121 LeuGlyAlaValSerTyrLeuHisSerLeuGlyIleValHisArgAspLeuLysProGlu 140  
  
QY 525 AACCTCCTCTATGCCACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTGGCCITG 584  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
141 AsnLeuLeuTyrAlaThrProPheGluAspSerLysIleMetValSerAspPheGlyLeu 160  
  
QY 585 TCCAAAATACAAGCTGGCAACATGCTAGGCACAGCCCTGTGGGACCCCGAGGATATGTGCC 644  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
161 SerLysIleGlnAlaGlyAsnMetLeuGlyThrAlaCysGlyThrProGlyTyrValAla 180  
  
QY 645 CCAGAGCTCCTGGAGCAGAAACCCCTACGGGAAGGCCGTAGATGTGTGGCCCTGGGTGTC 704  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
181 ProGluLeuLeuGluGlnLysProTyrGlyLysAlaValAspValTrpAlaLeuGlyVal 200  
  
QY 705 ATCTCCTACATCCTGCTGTGGGTACCCCCCTTCTATGATGAGAGCGATCCTGAATC 764  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
201 IleSerTyrIleLeuLeuCysGlyTyrProProPheTyrAspGluSerAspProGluLeu 220  
  
QY 765 TTCAGCCAGATTCTGAGGCCAGCTATGAGTTTGACTCCCTTTTGGGATGACATCTCA 824  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
221 PheSerGlnIleLeuArgAlaSerTyrGluPheAspSerProPheTrpAspAspIleSer 240  
  
QY 825 GAATCAGCCAAAGACTTCATTCGCCACCTTCTGGAACTGATCCCCAGAAGAGGTTTACC 884  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
241 GluSerAlaLysAspPheIleArgHisLeuLeuGluArgAspProGlnLysArgPheThr 260  
  
QY 885 TGCCAGCAGGCCCTACAGCATCTTTGGATCTCTGGGATGCAGCCTTCGATAGGGACATC 944  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
261 CysGlnGlnAlaLeuGlnHisLeuTrpIleSerGlyAspAlaAlaPheAspArgAspIle 280  
  
QY 945 CTGGGTTCTGTAGTGAGCAGATCCAGAAGAAATTTGCAGGACCCACTGGAAGCGTGCA 1004  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
281 LeuGlySerValSerGluGlnIleGlnLysAsnPheAlaArgThrHisTrpLysArgAla 300  
  
QY 1005 TTCAATGCCACATCATCTCTACGTACATCCGTACATCCGTAGCTGGGACAAAGCCAGAGGTCAG 1064  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
301 PheAsnAlaThrSerPheLeuArgHisIleArgLysLeuGlyGlnSerProGluGlyGlu 320  
  
QY 1065 GAGGCCTCCAGGCAGTGTATGACCCGTCATAGCCACCCAGGCCCTTGGGACTAGCCAGTCC 1124  
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
321 GluAlaSerArgGlnCysMetThrArgHisSerHisProGlyLeuGlyThrSerGlnSer 340  
  
QY 1125 CCCAAGTGG 1133  
Db |||||||||  
341 ProLysTrp 343  
  
RESULT 3  
O70150  
ID O70150 PRELIMINARY; PRT; 343 AA.  
AC O70150;  
DT 01-AUG-1998 (TrEMBLrel. 07, Created)  
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Ca2+/calmodulin-dependent protein kinase I beta 2.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=98070455; PubMed=9405489; DOI=10.1074/jbc.272.51.32704;  
RA Naito Y., Watanabe Y., Yokokura H., Sugita R., Nishio M., Hidaka H.;  
RT "Isoform-specific activation and structure diversity of calmodulin  
kinase I.";  
RL J. Biol. Chem. 272:32704-32708 (1997).  
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
DR EMBL; AB004267; BAA28263.1; -.  
DR HSSP; Q63450; 1A06.  
DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR011009; Kinase like.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
DR Pfam; PF00069; Pkinase; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00220; S\_TKC; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 343 AA; 38438 MW; 994D451D809A9D80 CRC64;

Alignment Scores:  
pred. No.: 4.65e-115 Length: 343  
Score: 1769.00 Matches: 341  
Percent Similarity: 99.42% Conservative: 0  
Best Local Similarity: 99.42% Mismatches: 2  
Query Match: 61.59% Indels: 0  
DB: 2 Gaps: 0

US-10-032-254A-1 (1-1554) x O70150 (1-343)

QY 105 ATGCTGCTGCTCAAGAAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAAG 164  
Db 1 MetLeuLeuLeuLysLysGlnThrGluAspIleSerSerValTyrGluIleArgGluLys 20

QY 165 CTGGGCTCGGGTGCCCTTCTCTGAGGTGATGCTGGCCAGGAAAGGGGCTCTGCTCATCTT 224  
Db 21 LeuGlySerGlyAlaPheSerGluValMetLeuAlaGlnGluArgGlySerAlaHisLeu 40

QY 225 GTGGCCCTCAAGTGCATTCCTCAAGAAAGCACCTTCGGGCAAGGAGGCCCTGTGGAGAAT 284  
Db 41 ValAlaLeuLysCysIleProLysLysAlaLeuArgGlyLysGluAlaLeuValGluAsn 60

QY 285 GAGATCGCGGTACTTCGAGAATCAGCCATCCCAACATTGTGGCTCTGGAGGACGTCCAT 344  
Db 61 GluIleAlaValLeuArgArgIleSerHisProAsnIleValAlaLeuGluAspValHis 80

QY 345 GAGAGTCCTTCTCATCTCTACTTGGCCATGGAGCTGGTAAACAGGTGGTGAACCTGTTGAC 404  
Db 81 GluSerProSerHisLeuTyrLeuAlaMetGluLeuValThrGlyGlyGluLeuPheAsp 100

QY 405 CGCATCATGGAGCGGGGCTCCTACACAGAGAAGGACGCGCAGCCACCTTGTAGGCGAGGTC 464  
Db 101 ArgIleMetGluArgGlySerTyrThrGluLysAspAlaSerHisLeuValGlyGlnVal 120

QY 465 CTTGGCGTGCTCCTACCTTCATAGCCTGGGCATCGTGCACCGGGACCTCAAGCCTGAA 524  
Db 121 LeuGlyAlaValSerTyrLeuHisSerLeuGlyIleValHisArgAspLeuLysProGlu 140

QY 525 AACCTCCTCTATGCCACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTGGCCTG 584  
Db 141 AsnLeuLeuTyrAlaThrProPheGluAspSerLysIleMetValSerAspPheGlyLeu 160

QY 585 TCCAAATACAAGCTGGCAACATGCTAGGCACAGCCTGTGGACCCCAGGATATGTGGCC 644  
Db 161 SerLysIleGlnAlaGlyAsnMetLeuGlyThrAlaCysGlyThrProGlyTyrValAla 180

QY 645 CCAGAGCTCCTGGAGCAGAAACCTTACGGGAAGGCCGTAGATGTGTGGGCCCTGGGTGTC 704  
Db 181 ProGluLeuLeuGluGlnLysProTyrGlyLysAlaValAspValTrpAlaLeuGlyVal 200

QY 705 ATCTCCTACATCCTGTGTGGGTACCCCTTCTATGATGAGAGCGATCCTGAACTC 764  
Db 201 IleSerTyrIleLeuLeuCysGlyTyrProProPheTyrAspGluSerAspProGluLeu 220

QY 765 TTCAGCCAGATTCTGAGGGCCAGCTATGAGTTTGACTCCCCCTTTTGGGATGACATCTCA 824  
Db 221 PheSerGlnIleLeuArgAlaSerTyrGluPheAspSerProPheTrpAspAspIleSer 240

QY 825 GAATCAGCCAAAGACTTCATTGCCCACTTCTTGAACGTGATCCCAGAGAGGTTTACC 884  
Db 241 GluSerAlaLysAspPheIleArgHisLeuLeuGluArgAspProGlnLysArgPheThr 260

QY 885 TGCCAGCAGGCCCTACAGCATCTTTGGATCTCTGGGATGCAGCCTTCGATAGGGACATC 944  
Db 261 CysGlnGlnAlaLeuGlnHisLeuTrpIleSerGlyAspAlaAlaLeuAspArgAspIle 280

QY 945 CTGGGTTCTGTCAGTGAGCAGATCCAGAAGATTTTGCAGGACCCACTGGAAGCGTGCA 1004  
Db 281 LeuGlySerValSerGluGlnIleGlnLysAsnPheAlaArgThrHisTrpLysArgAla 300

QY 1005 TTCAATGCCACATCATTCCTACGTCACTCCGTAAGCTGGGACAAAGCCACAGGGTGAG 1064  
Db 301 PheAsnAlaThrSerPheLeuArgHisIleArgLysLeuGlyGlnSerProGluGlyGlu 320

QY 1065 GAGGCCTCCAGGCAGTGTATGACCCGTCAATAGCCACCCAGGCCTTGGGACTAGCCAGTCC 1124  
Db 321 GluAlaSerArgGlnGlyMetThrArgHisSerHisProGlyLeuGlyThrSerGlnSer 340

QY 1125 CCCAAGTGG 1133  
Db 341 ProLysTrp 343

RESULT 4

O08767 PRELIMINARY; PRT; 342 AA.  
AC O08767;  
DT 01-JUL-1997 (TReMBLrel. 04, Created)  
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)  
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
DE Protein Kinase.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=97228532; PubMed=9074610; DOI=10.1016/S0167-4838(97)00004-6;  
RA Yokokura H., Terada O., Naito Y., Hidaka H.;  
RT "Isolation and comparison of rat cDNAs encoding Ca2+/calmodulin-  
RT dependent protein kinase I isoforms.";  
RL Biochim. Biophys. Acta 1338:8-12(1997).  
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
DR EMBL; D86556; BAA19879.1; -.  
DR HSSP; Q63450; 1A06.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR011009; Kinase like.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
DR Pfam; PF00069; Pkinase; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00220; S\_TKC; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 342 AA; 38463 MW; 546C464913E784A2 CRC64;

Alignment Scores:  
pred. No.: 5.13e-109 Length: 342  
Score: 1682.50 Matches: 334  
Percent Similarity: 86.79% Conservative: 1  
Best Local Similarity: 86.53% Mismatches: 4  
Query Match: 58.58% Indels: 47  
DB: 2 Gaps: 1



US-10-032-254A-1 (1-1554) x 008767 (1-342)

QY	105	ATGCTGCTGCTCAAGAAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAAG	164
Db	1	MetLeuLeuLeuLysLysGlnThrGluAspIleSerSerValTyrGluIleArgGluLys	20
QY	165	CTGGGCTCGGGTGCCTTCTCTGAGGTGATGCTGGCCCAAGAAAGGGCTCTGCTCATCTT	224
Db	21	LeuGlySerGlyAlaPheSerGluValMetLeuAlaGlnGluArgGlySerAlaHisLeu	40
QY	225	GTGGCCCTCAAGTGCATTCCCAAGAAAGCACTTCGGGGCAAGAGGCCCTGGTGGAGAAT	284
Db	41	ValAlaLeuLysCysIleProLysLysAlaLeuArgGlyLysGluAlaLeuValGluAsn	60
QY	285	GAGATCGGGTACTTCGCAGAATCAGCCATCCCAACATTGTGGCTCTGGAGGACGTCCT	344
Db	61	GluIleAlaValLeuArgArgIleSerHisProAsnIleValAlaLeuGluAspValHis	80
QY	345	GAGAGTCTTCTCATCTCTACTTGGCCATGGAGCTGGTAACAGSTGGTGAACCTGTTTGAC	404
Db	81	GluSerProSerHisLeuTyrLeuAlaMetGluLeuValThrGlyGlyGluLeuPheAsp	100
QY	405	CGCATCATGGAGCGGGCTCTTACACAGAGAAGGACGCCACCCACCTTGTAGGCAGGTC	464
Db	101	ArgIleMetGluArgGlySerTyrThrGluLysAspAlaSerHisLeuValGlyGlnVal	120
QY	465	CTTGGCGCTGCTCCTACCTTCATAGCCTGGGCATCGTGCACCGGACCTCAAGCCTGAA	524
Db	121	LeuGlyAlaValSerTyrLeuHisSerLeuGlyIleValHisArgAspLeuLysProGlu	140
QY	525	AACCTCTCTATGCCACACTTTTGAGGACTCCAAGATCATGCTCTCTGACTTTTGGCCTG	584
Db	141	AsnLeuLeuTyrAlaThrProPheGluAspSerLysIleMetValSerAspPheGlyLeu	160
QY	585	TCCAAAATACAAGCTGGCAACATGCTAGGCACAGCCTGTGGGACCCAGGATATGTGCC	644
Db	161	SerLysIleGlnAlaGlyAsnMetLeuGlyThrAlaCysGlyThrProGlyTyrValAla	180
QY	645	CCAGAGCTCCTGGAGCGAAGAACCTTACGGGAAGCCGTAGATGTGTGGGCCCTGGGTGC	704
Db	181	ProGluLeuLeuGluGlnLysProTyrGlyLysAlaValTrpAlaLeuGlyVal	200
QY	705	ATCTCTCATCCTGTGTGGGTACCCCTTCTATGATGAGAGCGATCCTGAACCTC	764
Db	201	IleSerTyrIleLeuLeuCysGlyTyrProPheTyrAspGluSerAspProGluLeu	220
QY	765	TTCAGCCAGATTCTGAGGCGCAGCTATGAGTTTGACTCCCCCTTTTGGGATGACATCTCA	824
Db	221	PheSerGlnIleLeuArgAlaSerTyrGluPheAspSerProPheTrpAspAspIleSer	240
QY	825	GAATCAGCCAAAGACTTCATTCCGCCACCTTCTGGAACGTGATCCCCAGAGAGGTTCCAC	884
Db	241	GluSerAlaLysAspPheIleArgHisLeuLeuGluArgAspProGlnLysArgPheThr	260
QY	885	TGCCAGAGGCCCTACAGCATCTTTGGATCTCTGGGGATGAGACCTTCGATAGGACATC	944
Db	261	CysGlnGlnAlaLeuGlnHisLeuTrpIleSerGlyAspAlaAlaLeuAspArgAspIle	280
QY	945	CTGGGTTCTGTGAGTGAGCAGATCCAGAAGAAATTTGCCAGGACCCACTTGAAGCGTGCA	1004
Db	281	LeuGlySerValSerGluGlnIleGlnLysAsnPheAlaArgThrHisTrpLysArgAla	300
QY	1005	TTCAATGCCACATCATCTTACGTCACATCCGTAAGCTGGGACAAAGCCAGAGGTTGAG	1064
Db	301	PheAsnAlaThrSerPheLeuArgHisIleArgLysLeuGlyGlnSerProGlu-----	318
QY	1065	GAGGCCTCCAGGCAGTGTATGACCCGTCATAGCCACCCAGGCCCTTGGGACTAGCCAGTCC	1124
Db	318	-----	318
QY	1125	CCCAAGTGTGAAAAACAGGTAGATGCCAAGGAAGGCCAAGTGAGTACTGACTCCCGGTTTT	1184
Db	318	-----	318

QY	1185	TCTTTCTCCAGCCCTTTTGGTGCTCTTTTCCTGGATCCTTGTCCTCCAGACTGGCCTCTGC	1244
Db	319	-----Ala--LeuLeuIleSerPheProAspProCysProProAspTrpProLeuL	335
QY	1245	TGGAAGTCTGAGA	1258
Db	335	eUGluSerProArg	339

RESULT 5  
 Q7T2H4

ID	Q7T2H4	PRELIMINARY;	PRT;	337 AA.
AC	Q7T2H4;			
DT	01-OCT-2003	(TrEMBLrel. 25, Created)		
DT	01-OCT-2003	(TrEMBLrel. 25, Last sequence update)		
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)		
DE	Ca2+/calmodulin-dependent protein kinase I-like protein.			
OS	Xenopus laevis (African clawed frog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;			
OC	Xenopodinae; Xenopus.			
OX	NCBI_TaxID=8355;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Kinoshita S., Sueyoshi N., Tsuge T., Suetake I., Tajima S.,			
RA	Kameshita I.;			
RL	Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.			
CC	-1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.			
DR	EMBL; AB098710; BAC78445.1; -.			
DR	HSSP; Q63450; 1A06.			
DR	GO; GO:0005524; F:ATP binding; IEA.			
DR	GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.			
DR	GO; GO:0016740; F:transferase activity; IEA.			
DR	GO; GO:0006468; P:protein amino acid phosphorylation; IEA.			
DR	InterPro; IPR011009; Kinase like.			
DR	InterPro; IPR000719; Prot_kinase.			
DR	InterPro; IPR002290; Ser_thr_pkinase.			
DR	InterPro; IPR008271; Ser_thr_pkin_AS.			
DR	Pfam; PF00069; Pkinase; I.			
DR	ProDom; PD000001; Prot_kinase; 1.			
DR	SMART; SM00220; S_TKc; 1.			
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.			
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.			
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.			
KW	ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.			
SQ	SEQUENCE 337 AA; 38405 MW; 92C417B65E7DE6DC CRC64;			

Alignment Scores:			
Pred. No.:	1.05e-87	Length:	337
Score:	1377.50	Matches:	260
Percent Similarity:	86.76%	Conservative:	35
Best Local Similarity:	76.47%	Mismatches:	36
Query Match:	47.96%	Indels:	9
DB:	2	Gaps:	2
US-10-032-254A-1 (1-1554) x Q7T2H4 (1-337)			
Qy	114	CTCAAGAAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAAGCTGGGCTCG	173
Db	7	VallYsLysLysIleGluAspIleAsnMetValTyrAsnIleLysGluLysLeuGlyAla	26
Qy	174	GGTGCCTTCTCTGAGGTGATGCTGGCCCAAGAGGGGCTCTGCTCATCTTGTGGCCTC	233
Db	27	GlyAlaPheSerGluValValLeuAlaGlnGluLysAsnSerGluArgLeuValAlaLeu	46
Qy	234	AAGTGCATTCCCAAGAACACTTCGGGGCAAGAGGCCCTGGTGGAGAATGAGATCGCG	293
Db	47	LysCysIleProLysLysAlaLeuArgGlyLysGluAlaValGluAsnGluIleAla	66
Qy	294	GTACTTCGAGAATCAGCCATCCCAACATTGTGGCTCTGGAGGACGTCCATGAGTCCT	353
Db	67	ValLeuLysLysIleThrHisGlnAsnIleValSerLeuAspAspIleTyrGluSerPro	86

QY 354 TCTCATCTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAACTGTTTGACCGCATCATG 413  
:::|||||  
Db 87 ThrHisLeuTyrLeuAlaMetGluLeuValThrGlyGlyGluLeuPheAspArgIleIle 106  
:::|||||  
QY 414 GAGCGGGCTCCTACACAGAGAAGGACGCCACCTTGTAGGGCAGGTCTTGGCGCT 473  
|||||  
Db 107 GluArgGlyTyrTyrThrGluLysAspAlaSerGlnLeuIleGlyGlnValLeuAspAla 126  
|||||  
QY 474 GTCTCTACCTTCATAGCTGGGCATCGTGCCACCGGACCTCAAGCCTGAAAACCTCCTC 533  
|||  
Db 127 ValGlnTyrLeuHisAsnMetGlyIleValHisArgAspLeuLysProGluAsnLeuLeu 146  
|||||  
QY 534 TATGCCACACCTTTTGAGACTCCAAGATCATGCTCTGACTTTGGCCTGTCCAAATA 593  
|||||  
Db 147 TyrAlaThrProPheGluAspSerLysIleMetIleSerAspPheGlyLeuSerLysPhe 166  
|||||  
QY 594 CAAGCTGGCAACATGCTAGGCACAGCCTGTGGGACCCAGGATATGTGGCCCCAGAGCTC 653  
:::|||||  
Db 167 GluAspSerGlyMetMetAlaThrAlaCysGlyThrProGlyTyrValAlaProGluLeu 186  
:::|||||  
QY 654 CTGGAGCAGAAACCCTACGGGAAGCCGTAGATGTGTGGGCCCTGGGTGTCTCTCTAC 713  
|||||  
Db 187 LeuGluGlnLysProTyrGlyLysAlaValAspValTrpAlaIleGlyValIleSerTyr 206  
|||||  
QY 714 ATCTCTGTGTGGGTACCCCCCTTCTATGATGAGAGCGATCCTGAACCTCTCAGCCAG 773  
|||||  
Db 207 IleLeuLeuCysGlyTyrProProPheTyrAspGluAsnAspSerGluLeuPheAsnGln 226  
|||||  
QY 774 ATTCTGAGGGCCAGCTATGAGTTTGACTCCCCCTTTTGGGATGACATCTCAGAATCAGCC 833  
|||||  
Db 227 IleLeuLysAlaGluTyrGluPheAspSerProTyrTrpAspAspIleSerGluSerAla 246  
|||||  
QY 834 AAAGACTTCATTCCGCCACCTTCTGGAACGTGATCCCCCAGAGAGGTTTCACCTGCCAGCAG 893  
|||||  
Db 247 LysAspPheIleArgHisLeuLeuGluArgGluProGluLysArgLeuThrCysGluGln 266  
|||||  
QY 894 GCCCTACAGCATCTTTGGATCTCTGGGGATGCAGCCCTTCGATAGGGACATCTCGGTTCT 953  
|||||  
Db 267 AlaLeuGlnHisProTrpIleCysGlyAspThrAlaLeuGluArgAspIleHisGlySer 286  
|||||  
QY 954 GTCAGTGAGCAGATCCAGAAGAATTTTGCCAGGACCCACTGGAAGCGTGCATTCAATGCC 1013  
|||||  
Db 287 ValSerGluGlnIleGlnLysAsnPheAlaArgSerGlnTrpLysArgAlaPheAsnAla 306  
|||||  
QY 1014 ACATCATCTCTACGTACATCCGTAAGCTGGGACAAAGCCACAGAGGTTGAGGAGCCCTCC 1073  
|||||  
Db 307 ThrSerPheLeuArgHisIleThrLysMetGlyGlnSerAlaGluThrGluGlu----- 324  
|||||  
QY 1074 AGGCAGTGATGACCCCGTCATAGCCACCCAGGCCCTTGGGACTAGCCAGTCCCCCAAGTGG 1133  
|||  
Db 325 -----HisHisGlyGluPro-----ValProGluGluLysAspLysTrp 337  
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RESULT 6  
Q6P2M8  
ID Q6P2M8 PRELIMINARY; PRT; 241 AA.  
AC Q6P2M8;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE PNCK protein.  
GN Name=PNCK;  
OS Homo sapiens (Human).  
OC • Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxId=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnersch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Strausberg R.;  
RL Submitted (DEC-2003) to the EMBL/GenBank/DBDJ databases.  
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
DR EMBL; BC064422; AAHe4422.1; -.  
DR HSSP; Q63450; 1A06.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR011009; Kinase like.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
DR Pfam; PF00069; Pkinase; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00220; S\_TKC; 1.  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 241 AA; 27160 MW; 6AA7E6AFEOCEB409 CRC64;

Alignment Scores:

Pred. No.:	6.68e-76	Length:	241
Score:	1208.00	Matches:	228
Percent Similarity:	95.44%	Conservative:	2
Best Local Similarity:	94.61%	Mismatches:	11
Query Match:	42.06%	Indels:	0
DB:	2	Gaps:	0

US-10-032-254A-1 (1-1554) x Q6P2M8 (1-241)

QY	411	ATGGAGCGGGCTCTACACAGAGAAGGACGCCAGCCACCTTGTAGGGCAGGTCTTGGC	470
Db	1	MetGluArgGlySerTyrThrGluLysAspAlaSerHisLeuValGlyGlnValLeuGly	20
QY	471	GCTGTCTCCTACCTTCATAGCCTGGGCATCGTGCACCGGACCTCAAGCCTGAAAACCTC	530
Db	21	AlaValSerTyrLeuHisSerLeuGlyIleValHisArgAspLeuLysProGluAsnLeu	40
QY	531	CTCTATGCCACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTGGCCTGTCCAAA	590
Db	41	LeuTyrAlaThrProPheGluAspSerLysIleMetValSerAspPheGlyLeuSerLys	60
QY	591	ATACAAGCTGGCAACATGCTAGGCACAGCCTGTGGGACCCCGAGGATATGTGGCCCCAGAG	650
Db	61	IleGlnAlaGlyAsnMetLeuGlyThrAlaCysGlyThrProGlyTyrValAlaProGlu	80
QY	651	CTCCTGGAGCAGAAACCCTACGGGAAGCCGTAGATGTGTGGCCCTGGGTGTCATCTCC	710
Db	81	LeuLeuGluGlnLysProTyrGlyLysAlaValAspValTrpAlaLeuGlyValIleSer	100
QY	711	TACATCCTGCTGTGGGTACCCCCCTTCTATGATGAGAGCGATCCTGAACTCTTCAGC	770
Db	101	TyrIleLeuLeuCysGlyTyrProProPheTyrAspGluSerAspProGluLeuPheSer	120

QY 771 CAGATTCTGAGGCCAGCTATGAGTTTGACTCCCCCTTTTGGGATGACATCTCAGAAATCA 830  
Db |||||||  
QY 121 GlnIleLeuArgAlaSerTyrGluPheAspSerProPheTrpAspAspIleSerGluSer 140  
Db |||||||  
QY 831 GCCAAAGACTTCATTGCGCCACCTTCTGTGAACGTGATCCCCACAAGAGGTTTCACCTGCCAG 890  
Db |||||||  
QY 141 AlaLysAspPheIleArgHisLeuLeuGluArgAspProGlnLysArgPheThrCysGln 160  
Db |||||||  
QY 891 CAGGCCCTACAGCATCTTTGGATCTCTGGGATGCGCCCTTCGATAGGGACATCCTGGGT 950  
Db |||||||  
QY 161 GlnAlaLeuArgHisLeuTrpIleSerGlyAspThrAlaPheAspArgAspIleLeuGly 180  
Db |||||||  
QY 951 TCTGTCACTGAGCAGATCCAGAAAGATTTTGCCAGGACCCACTGGAAGCGTGCATTCAAT 1010  
Db |||||||  
QY 181 SerValSerGluGlnIleArgLysAsnPheAlaArgThrHisTrpLysArgAlaPheAsn 200  
Db |||||||  
QY 1011 GCCACATCATTCCTACGTCACATCCGTAAGCTGGGACAAAGCCAGAGGGTGAGGAGGCC 1070  
Db |||||||  
QY 201 AlaThrSerPheLeuArgHisIleArgLysLeuGlyGlnIleProGluGlyGluGlyAla 220  
Db |||||||  
QY 1071 TCCAGGCAGTGTATGACCCGTCATAGCCACCCAGGCCCTTGGGACTAGCCAGTCCCCCAAG 1130  
Db |||||||  
QY 221 SerGluGlnGlyMetAlaArgHisSerHisSerGlyLeuArgAlaGlyGlnProProLys 240  
QY 1131 TGG 1133  
Db |||  
Db 241 Trp 241

RESULT 7  
Q8AVN4  
ID Q8AVN4 PRELIMINARY; PRT; 378 AA.  
AC Q8AVN4;  
DT 01-MAR-2003 (TREMBLrel. 23, Created)  
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Camk1-prov protein.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
OC xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
RA Richardson P.;  
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus

RT initiative.";  
RL Dev. Dyn. 225:384-391(2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RA Klein S., Strausberg R.;  
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
DR EMBL; BC041721; AAH41721.1; -.  
DR HSSP; Q63450; 1A06.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR011009; Kinase Like.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR002290; Ser\_thr\_kinase.  
DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
DR Pfam; PF00069; Pkinase; 1.  
DR proDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00220; S\_TKc; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 378 AA; 42567 MW; 066A78028EF2DAA6 CRC64;

Alignment Scores:  
Pred. No.: 1.12e-75 Length: 378  
Score: 1205.50 Matches: 232  
Percent Similarity: 79.05% Conservative: 51  
Best Local Similarity: 64.80% Mismatches: 50  
Query Match: 41.97% Indels: 25  
DB: 2 Gaps: 5

US-10-032-254A-1 (1-1554) x Q8AVN4 (1-378)

QY 117 AAGAAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAAGCTGGGCTCGGT 176  
Db |||||::: ||||||| ::||| ||||| |||||::: |||||  
11 LysLysArgAlaGluAspIleArgAspIleTyrGluPheArgGluValLeuGlyThrGly 30  
QY 177 GCCTTCTCTGAGGTGATGTGGCCCGAGGAAAGGGGCTCTGCTCATCTTGTGGCCCTCAAG 236  
Db |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||  
31 AlaPheSerGluValValLeuAlaGluGluLysLysThrGlnLysLeuValAlaIleLys 50  
QY 237 TGCATTCCCAAGAACGACTTCGGGGCAAGGAGGCCCTCGTGAGAAATGAGATCGCGGTA 296  
Db |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||  
51 CysIleProLysLysAlaLeuGluGlyLysGluThrSerIleGluAsnGluIleAlaVal 70  
QY 297 CTTTCGAGAATCAGCCATCCCAACATTGTGGCTCTGGAGGACGTCCATGAGAGTCCTTCT 356  
Db |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||  
71 LeuArgLysIleLysHisThrAsnIleValSerLeuGluAspIleTyrAspSerArgSer 90  
QY 357 CATCTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAACCTTTGACCGCATCATGGAG 416  
Db |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||  
91 HisLeuTyrLeuIleMetGlnLeuValSerGlyGlyGluLeuPheAspArgIleValGlu 110  
QY 417 CGGGGCTCTACACAGAGGACGCCAGCCACCTTGTAGGGCAGGTCCTTGGCGCTGTC 476  
Db |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||  
111 LysGlyPheTyrThrGluLysAspAlaSerGlnLeuLysGlnIleLeuAspAlaVal 130  
QY 477 TCCTACCTTCATAGCTGGGCATCGTGCACCGGGACCTCAAGCCTGAAAACCTCCTCTAT 536  
Db |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||  
131 LysTyrLeuHisAspMetGlyIleValHisArgAspLeuLysProGluAsnLeuLeuTyr 150  
QY 537 GCCACACCTTTTGAGGACTCCAAAGATCATGGTCTCTGACTTTGGCCTGTCCAAAATACAA 596  
Db |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||  
151 TyrSerIleAspGluAspSerLysIleMetIleSerAspPheGlyLeuSerLysIleGlu 170  
QY 597 ---GCTGGCAACATGCTAGGCACAGCCTGTGGGACCCAGGATATGTGGCCCCAGAGCTC 653  
Db |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||::: |||||  
171 GlySerGlySerValMetSerThrAlaCysGlyThrProGlyTyrValAlaProGluVal 190





```
Db      311 ThrAlaValIleArgHisMetArgLysLeuGlnLeuGlyThrSerGlnGluGly------ 328
QY      1068 GCCTCCAGGCAGTGTATGACCCCGTCATAGCCACCCAGGCCCTTGGGACTAGCCAGTCCCCC 1127
Db      329 -----ProGlyGlnThrThrProThrSerPro 337
QY      1128 AAGTGGTGAACACAGGTAGATGCCAAGGAAGGCCAAGTGGACTGACTCCCGGT 1181
Db      338 -----CysHisGly-----AsnLeuLeuMetProGly 346

RESULT 9
Q6GM90
ID Q6GM90      PRELIMINARY;      PRT;      395 AA.
AC Q6GM90;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE MGC82022 protein.
GN Name=MGC82022;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC -! SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL; BC074183; AAH74183.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR011009; Kinase_like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
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DR      InterPro; IPR008271; Ser_thr_pkin_AS.
DR      InterPro; IPR001245; Tyr_pkinase.
DR      Pfam; PF00069; Pkinase; 1.
DR      ProDom; PD000001; Prot_kinase; 1.
DR      SMART; SM00220; S_TKC; 1.
DR      SMART; SM00219; TyrKc; 1.
DR      PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR      PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR      PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 395 AA; 43896 MW; 4C78B8BF828A2CC4 CRC64;

Alignment Scores:
Pred. No.:      9.19e-75      Length:      395
Score:          1192.50      Matches:      234
Percent Similarity:      77.08%      Conservative:      62
Best Local Similarity:      60.94%      Mismatches:      62
Query Match:      41.52%      Indels:      26
DB:              2      Gaps:      6

US-10-032-254A-1 (1-1554) x Q6GM90 (1-395)
QY      117 AAGAAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAAGCTGGGTCGGGT 176
Db      14 LysLysGlnValGluAspIleLysArgMetPheGlnPheLysGluValLeuGlyThrGly 33
QY      177 GCCTTCTCTGAGGTGATGTGGCCCGCCAGGAAAGGGGCTCTGCTCATCTTGTGGCCCTCAAG 236
Db      34 AlaPheSerGluValValLeuAlaGluGluLysGluThrGlyLysLeuPheAlaValLys 53
QY      237 TGCATTCCCAAGAAAGCACTTCGGGGCAAGGAGGCCCTGGTGAGAAATGAGATCGCGGTA 296
Db      54 CysIleProLysLysAlaLeuLysGlyLysGluSerIleGluAsnGluIleAlaVal 73
QY      297 CTTCGCAGAATCAGCCATCCCAACATTGTGGCTCTGGAGGACGTCCTATGAGAGTCCTTCT 356
Db      74 LeuArgLysIleLysHisGluAsnIleValAlaLeuGluAspIleTyrGluSerProSer 93
QY      357 CATCTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAACCTGTTTGACCGCATCATGGAG 416
Db      94 HisLeuTyrLeuValMetGlnLeuValSerGlyGlyGluLeuPheAspArgIleValGlu 113
QY      417 CGGGGCTCCTACACAGAGAAGGACGCCAGCCACCTTGTAGGGCAGGTCCCTTGGCGCTGTC 476
Db      114 LysGlyPheTyrThrGluLysAspAlaSerThrLeuIleArgGlnValLeuAspAlaVal 133
QY      477 TCCTACCTTCATAGCCTGGGCATCGTGCACCGGGACCTCAAGCCTGAAAACCTCCTCTAT 536
Db      134 SerTyrLeuHisArgLeuGlyIleValHisArgAspLeuLysProGluAsnLeuLeuTyr 153
QY      537 GCCACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTGGCCTGTCCAAATACAA 596
Db      154 PheSerGlnValGluGluSerLysIleMetIleSerAspPheGlyLeuSerLysMetGlu 173
QY      597 GCT---GGCAACATGCTAGGCACAGCCTGTGGGACCCAGGATATGTGGCCCCAGAGCTC 653
Db      174 GlyLysGlyAspValMetSerThrAlaCysGlyThrProGlyTyrValAlaProGluVal 193
QY      654 CTGGAGCAGAAACCCCTACGGGAAGCCGCTAGATGTGTGGGCCCTGGGTGTCATCTCCTAC 713
Db      194 LeuAlaGlnLysProTyrSerLysAlaValAspCysTrpSerIleGlyValIleAlaTyr 213
QY      714 ATCTGTGTGTGGGTACCCCCCTTCTATGATGAGAGCGATCCTGAACTCTTCAGCCAG 773
Db      214 IleLeuLeuCysGlyTyrProProPheTyrAspGluAsnAspSerArgLeuPheGluGln 233
QY      774 ATTCTGAGGGCCAGCTATGAGTTTGACTCCCCCTTTGGGATGACATCTCAGAAATCAGCC 833
Db      234 IleLeuLysAlaAspTyrGluPheAspSerProTyrTrpAspAspIleSerGluSerAla 253
QY      834 AAAGACTTTCATTCGCCACCTTCTGGAACGTGATCCCCAGAAAGAGTTTCACCTGCCAGCAG 893
Db      254 LysAspPheIleGlnAsnLeuMetGluLysAspProAsnLysArgTyrThrCysGluGln 273
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QY 894 GCCCTACAGCATCTTTGGATCTCTGGGATGCAGCCTTCGATAGGACATCCTGGTTCT 953
|||||:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 274 AlaLeuArgHisProTrpIleAlaGlyAspThrAlaLeuCysLysAsnIleHisGluSer 293
|||||:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 954 GTCAGTGACGATCCAGAAGAATTTTGCAGGACCCACTGGAAGCGTGCAATCAATGCC 1013
|||||:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 294 ValSerAlaGlnIleArgLysAsnPheAlaLysSerLysTrpArgGlnAlaPheAsnAla 313
|||||:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1014 ACATCATCTCTACGTACATCCGTAAG-----CTGGGACAAAGCCAGAGCGGTGAGGAG 1067
|||||:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 314 ThrAlaValValArgHisMetArgLysLeuHisLeuGlySerSerGlnAspSerSerAsn 333
|||||:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1068 GCCTCCAGGCAGTGATGACCCGTATAGCCACCCAGGCGCTTGGGACTAGCCAGTCCC-- 1125
|||||:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 334 ValSer-GlyGlyAsnSerPro-----AlaSerProLe 344
|||||:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1126 -CCAAGTGGTGAAAAACCAGGTAGATGCCAAGGAGGCCAAGTGGACTGACTCCCGGTTTT 1184
|||||:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 344 uProAspGlyThrSerArgLysAspCysLysPro----- 355
|||||:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1185 TCCTTCTCCAGCCCTTTTGGTCTCTTTCCTGGA-----TCCTTGCTCCTCCAGACTGGC 1238
|||||:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 356 ----ProSerThrProTyrSerPheLeuSerGlyValSerSerAlaSerSerAlaIleSe 374
|||||:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 1239 CTCTGCTGGA 1248
|||||:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 374 rAlaValGly 377
|||||:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 10
KCC1_MOUSE
ID KCC1_MOUSE STANDARD; PRT; 374 AA.
AC Q91Y58;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase type I (EC 2.7.1.123) (CaM
kinase I).
GN Name=Camk1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC -!- FUNCTION: Phosphorylates synapsin I (By similarity).
CC -!- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
CC -!- ENZYME REGULATION: Activated by Ca(2+)/calmodulin. Must be
phosphorylated to be maximally active.
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. CamK
subfamily.
```

```
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; BC014825; AAH14825.1; -.
DR HSSP; Q63450; 1A06.
DR MGD; MGI:1098535; Camk1.
DR GO; GO:0006913; P:nucleocytoplasmic transport; IDA.
DR GO; GO:0007165; P:signal transduction; IDA.
DR InterPro; IPR011009; Kinase like.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; Pkinase; 1.
DR ProDom; PD000001; Prot_kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Calmodulin-binding; Phosphorylation;
KW Serine/threonine-protein kinase; Transferase.
FT DOMAIN 20 276 protein kinase.
FT NP_BIND 287 321 Calmodulin-binding (By similarity).
FT BINDING 26 34 ATP (By similarity).
FT BINDING 49 49 ATP (By similarity).
FT ACT_SITE 141 141 Proton acceptor (By similarity).
FT MOD_RES 177 177 Phosphothreonine (by autocatalysis) (By
similarity).
SQ SEQUENCE 374 AA; 41624 MW; 37889CDA717D3AB2 CRC64;

Alignment Scores:
Pred. No.: 1.72e-74 Length: 374
Score: 1188.50 Matches: 221
Percent Similarity: 85.53% Conservative: 51
Best Local Similarity: 69.50% Mismatches: 43
Query Match: 41.38% Indels: 3
DB: 1 Gaps: 2

US-10-032-254A-1 (1-1554) x KCC1_MOUSE (1-374)
QY 120 AAACAGACGGAGACATCAGCAGTGTCTATGATCCGGGAGAGCTGGGCTCGGTGCC 179
|||||:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 11 LysGlnAlaGluAspIleArgAspIleTyrAspPheArgAspValLeuGlyThrGlyAla 30
|||||:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 180 TTCTCTGAGGTGATGCTGGCCCGCCAGGAAAGGGCTCTGCTCATCTTTGGCCCTCAAGTGC 239
|||||:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 31 PheSerGluValIleLeuAlaGluAspLysArgThrGlnLysLeuValAlaIleLysCys 50
|||||:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 240 ATTCCCAAGAAAGCACTTCGGGGCAAGGAGGCCCTGGTGGAGAATGAGATCGCGGTACTT 299
|||||:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 51 IleAlaLysLysAlaLeuGluGlyLysGluGlySerMetGluAsnGluIleAlaValLeu 70
|||||:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 300 CGCAGAATCAGCCATCCCAACATTGTGGCTCTGGAGGACGTCCATGAGAGTCCTTCTCAT 359
|||||:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 71 HisLysIleLysHisProAsnIleValAlaLeuAspAspIleTyrGluSerGlyGlyHis 90
|||||:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 360 CTCTACTTGGCCCTGGAGCTGGTAACAGGTGGTGAACACTGTTTGACCGCATCATGGAGCGG 419
|||||:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 91 LeuTyrLeuIleMetGlnLeuValSerGlyGlyGluLeuPheAspArgIleValGluLys 110
|||||:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 420 GGCTCCTACACAGAGAAGGACGCCACCTGTAGGGCAGGTCCTTGGCGCTGTCTCC 479
|||||:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 111 GlyPheTyrThrGluArgAspAlaSerArgLeuIlePheGlnValLeuAspAlaValLys 130
|||||:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 480 TACCTTCATAGCCTGGGCATCGTGCACCGGAGACCTCAAGCCTGAAAACCTCCTCTATGCC 539
|||||:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 131 TyrLeuHisAspLeuGlyIleValHisArgAspLeuLysProGluAsnLeuLeuTyrTyr 150
|||||:|:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
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FT STRAND      147      149      155
FT TURN        154      155
FT STRAND      158      160
FT TURN        183      184
FT HELIX       187      190
FT TURN        191      192
FT TURN        197      197
FT HELIX       198      213
FT HELIX       223      231
FT TURN        232      233
FT TURN        239      244
FT HELIX       247      256
FT HELIX       261      263
FT HELIX       267      272
FT TURN        274      277
FT HELIX       287      297
FT TURN        302      304
FT STRAND      307      307
FT HELIX       309      315
SQ SEQUENCE    374 AA; 41638 MW; 37889B3DEF033AB2 CRC64;
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Alignment Scores:  
Pred. No.: 1.72e-74 Length: 374  
Score: 1188.50 Matches: 221  
Percent Similarity: 85.53% Conservative: 51  
Best Local Similarity: 69.50% Mismatches: 43  
Query Match: 41.38% Indels: 3  
DB: 1 Gaps: 2

US-10-032-254A-1 (1-1554) x KCC1\_RAT (1-374)

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QY 120 AAACAGACGGAGGACATCAGCAGTGTCTATGAGATCCGGGAGAAGCTGGGTCGGGTGCC 179
Db 11 LysGlnAlaGluAspIleArgAspIleTyrAspPheArgAspValLeuGlyThrGlyAla 30
QY 180 TTCTCTGAGGTGATGTGGCCCGCCAGGAAAGGGGCTCTGCTCATCTTGTGGCCCTCAAGTGC 239
Db 31 PheSerGluValIleLeuAlaGluAspLysArgThrGlnLysLeuValAlaIleLysCys 50
QY 240 ATTCCCAAGAAAGCACTTTCGGGCAAGGAGGCCCTCGTGAGAAATGAGATCGCGGTACTT 299
Db 51 IleAlaLysLysAlaLeuGluGlyLysGluGlySerMetGluAsnGluIleAlaValLeu 70
QY 300 CGCAGAATCAGCCATCCCAACATTGTGGCTCTGGAGGACGTCCATGAGAGTCCTCTCAT 359
Db 71 HisLysIleLysHisProAsnIleValAlaLeuAspAspIleTyrGluSerGlyGlyHis 90
QY 360 CTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAATGTTTGACCGCATCATGGAGCGG 419
Db 91 LeuTyrLeuIleMetGlnLeuValSerGlyGlyGluLeuPheAspArgIleValGluLys 110
QY 420 GGCTCCTACACAGAGAAGACGCGCCAGCCACCTTGTAGGGCAGGTCTCTGGCGGTCTCTCC 479
Db 111 GlyPheTyrThrGluArgAspAlaSerArgLeuIlePheGlnValLeuAspAlaValLys 130
QY 480 TACCTTCATAGCCTGGGCATCGTGCACCGGGACCTCAAGCCTGAAACCTCCTCTATGCC 539
Db 131 TyrLeuHisAspLeuGlyIleValHisArgAspLeuLysProGluAsnLeuLeuTyrTyr 150
QY 540 ACACCTTTTGAGGACTCCAGATCATGGTCTCTGACTTGGCCTGTCCAAATACAA--- 596
Db 151 SerLeuAspGluAspSerLysIleMetIleSerAspPheGlyLeuSerLysMetGluAsp 170
QY 597 GCTGGCAACATGCTAGGCACAGCCTGTGGGACCCAGGATATGTGGCCCGCAGAGTCCTG 656
Db 171 ProGlySerValLeuSerThrAlaCysGlyThrProGlyTyrValAlaProGluValLeu 190
QY 657 GAGCAGAAACCTTACGGGAAGCCGTAGATGTGTGGGCCCTGGGTGTCATCTCTACATC 716
Db 191 AlaGlnLysProTyrSerLysAlaValAspCysTrpSerIleGlyValIleAlaTyrIle 210
QY 717 CTGCTGTGTGGGTACCCCTTCTATGATGAGAGCGCATCTGAACTCTTCAGCCAGATT 776
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Db 211 LeuLeuCysGlyTyrProPheTyrAspGluAsnAspAlaLysLeuPheGluGlnIle 230
QY 777 CTGAGGGCCAGCTATGAGTTTGACTCTCCCTTTTGGGATGACATCTCAGAAATCAGCCAAA 836
Db 231 LeuLysAlaGluTyrGluPheAspSerProTyrTyrAspAspIleSerAspSerAlaLys 250
QY 837 GACTTCATTGCCACCTTCTGGAAACGTATCCCCAGAGAGGTTTCACCTGCAGCAGGCC 896
Db 251 AspPheIleArgHisLeuMetGluLysAspProGluLysArgPheThrCysGluGlnAla 270
QY 897 CTACAGCATCTTTGGATCTCTGGGATGCAGCCTTCGATAGGGACATCCTGGGTTCTGTC 956
Db 271 LeuGlnHisProTrpIleAlaGlyAspThrAlaLeuAspLysAsnIleHisGlnSerVal 290
QY 957 AGTGAGCAGATCCAGAAGAATTTTGCAGGAGCCCACTGGAAGCGTGCATTCAATGCCACA 1016
Db 291 SerGluGlnIleLysLysAsnPheAlaLysSerLysTrpLysGlnAlaPheAsnAlaThr 310
QY 1017 TCATTCCCTACGTACATCCGTAAG-----CTGGGACAAAGCCAGAGGGTGAG 1064
Db 311 AlaValValArgHisMetArgLysLeuGlnLeuGlyThrSerGlnGluGlyGln 328

RESULT 12
KCC1_HUMAN
ID KCC1_HUMAN STANDARD; PRT; 370 AA.
AC Q140I2;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Calcium/calmodulin-dependent protein kinase type I (EC 2.7.1.123) (CaM
DE kinase I).
GN Name=CaMK1;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-49.
RX MEDLINE=95369239; PubMed=7641687;
RA Haribabu B., Hook S.S., Selbert M.A., Goldstein E.G., Tomhave E.D.,
RA Edelman A.M., Snyderman R., Means A.R.;
RT "Human calcium-calmodulin dependent protein kinase I: cDNA cloning,
RT domain structure and activation by phosphorylation at threonine-177 by
RT calcium-calmodulin dependent protein kinase I kinase.";
RL EMBO J.14:3679-3686(1995).
RN [2]
RP SEQUENCE OF 1-9.
RC TISSUE=Platelet;
RX MEDLINE=22608298; PubMed=12665801; DOI=10.1038/nbt810;
RA Gevaert K., Goethals M., Martens L., Van Damme J., Staes A.,
RA Thomas G.R., Vandekerckhove J.;
RT "Exploring proteomes and analyzing protein processing by mass
RT spectrometric identification of sorted N-terminal peptides.";
RL Nat. Biotechnol. 21:566-569(2003).
CC -!- FUNCTION: Phosphorylates synapsin I.
CC -!- CATALYTIC ACTIVITY: ATP + protein = ADP + O-phosphoprotein.
CC -!- ENZYME REGULATION: Activated by Ca(2+)/calmodulin. Must be
CC phosphorylated to be maximally active.
CC -!- SUBUNIT: Monomer.
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family. CaMK
CC subfamily.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC -----
CC EMBL; L41816; AAA99458.1; -.
CC PIR; S57347; S57347.
CC
DR
DR
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DR HSSP; Q63450; 1A06.  
DR Genew; HGNC:1459; CAMK1.  
DR MIM; 604998; -.  
DR GO; GO:0004685; F:calcium/calmodulin-dependent protein kinase. . .; TAS.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; TAS.  
DR GO; GO:0007165; P:signal transduction; TAS.  
DR InterPro; IPR011009; Kinase\_like.  
DR InterPro; IPR00719; Prot\_kinase.  
DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
DR InterPro; IPR022290; Ser\_thr\_pkinase.  
DR Pfam; PF00069; Pkinase; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00220; S\_TKC; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Calmodulin-binding; Direct protein sequencing;  
KW Phosphorylation; Serine/threonine-protein kinase; Transferase.  
FT DOMAIN 20 276 Protein kinase.  
FT DOMAIN 287 321 Calmodulin-binding (By similarity).  
FT NP\_BIND 26 34 ATP (By similarity).  
FT BINDING 49 49 ATP.  
FT ACT\_SITE 141 141 Proton acceptor (By similarity).  
FT MOD\_RES 177 177 Phosphothreonine (by autocatalysis).  
FT MUTAGEN 49 49 K->A: Loss of activity.  
SQ SEQUENCE 370 AA; 41337 MW; 57FA20ECE00FA76C CRC64;

Alignment Scores:

Pred. No.: 3.27e-74 Length: 370  
Score: 1184.50 Matches: 220  
Percent Similarity: 85.53% Conservative: 52  
Best Local Similarity: 69.18% Mismatches: 43  
Query Match: 41.24% Indels: 3  
DB: 1 Gaps: 2

US-10-032-254A-1 (1-1554) x KCC1\_HUMAN (1-370)

QY 120 AAACAGACGGAGGACATCCAGCAGTGTCTATGAGATCCGGGAGAAGCTGGGCTCGGTGCC 179  
Db 11 LysGlnAlaGluAspIleArgAspIleTyrAspPheArgAspValLeuGlyThrGlyAla 30  
QY 180 TTCTCTGAGGTGATGCTGGCCACGAAAGGGCTCTGCTCATCTTGTGGCCCTCAAGTGC 239  
Db 31 PheSerGluValIleLeuAlaGluAspLysArgThrGlnLysLeuValAlaIleLysCys 50  
QY 240 ATTCCTCAAGAAAGCACTTCGGGCAAGGAGGCCCTGGTGGAGAATGAGATCGCGGTACTT 299  
Db 51 IleAlaLysGluAlaLeuGluGlyLysGluGlySerMetGluAsnGluIleAlaValLeu 70  
QY 300 CGCAGAATCAGCCATCCCAACATGTGGCTCTGGAGGACGTCATGAGATCCTTCTCAT 359  
Db 71 HisLysIleLysHisProAsnIleValAlaLeuAspAspIleTyrGluSerGlyGlyHis 90  
QY 360 CTCTACTTGGCCATGGAGCTGTTAACAGGTGGTGAACCTGTTGACCGCATCATGGACGG 419  
Db 91 LeuTyrLeuIleMetGlnLeuValSerGlyGlyGluLeuPheAspArgIleValGluLys 110  
QY 420 GGCTCTACACAGAGAAGGACGCCAGCCACCTTGTAGGGAGGTCTTGGCGCTGTCTCC 479  
Db 111 GlyPheTyrThrGluArgAspAlaSerArgLeuIlePheGlnValLeuAspAlaValLys 130  
QY 480 TACCTTCATAGCCTGGGCATCGTCACCGGGACCTCAAGCCTGAAACCTCCTCTATGCC 539  
Db 131 TyrLeuHisAspLeuGlyIleValHisArgAspLeuLysProGluAsnLeuLeuTyrTyr 150  
QY 540 ACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTGGCTGTCCAAATACAA--- 596  
Db 151 SerLeuAspGluAspSerLysIleMetIleSerAspPheGlyLeuSerLysMetGluAsp 170  
QY 597 GCTGGCAACATGCTAGGCACAGCCTGTGGGACCCCGAGATATGTGGCCCCCAGAGCTCTG 656  
Db 171 ProGlySerValLeuSerThrAlaCysGlyThrProGlyTyrValAlaProGluValLeu 190

QY 657 GAGCAGAAACCCCTACGGGAAGCCGTAGATGTGTGGCCCTGGGTGTCATCTCTACATC 716  
Db 191 AlaGlnLysProTyrSerLysAlaValAspCysTrpSerIleGlyValIleAlaTyrIle 210  
QY 717 CTGCTGTGTGGGTACCCCCCTTCTATGATGAGAGCGCATCCTGAACCTTTCAGCCAGATT 776  
Db 211 LeuLeuCysGlyTyrProPheTyrAspGluAsnAspAlaLysLeuPheGluGlnIle 230  
QY 777 CTGAGGGCCAGCTATGAGTTTGACTCCCCCTTTTGGGATGACATCTCAGAAATCAGCAAA 836  
Db 231 LeuLysAlaGluTyrGluPheAspSerProTyrTrpAspAspIleSerAspSerAlaLys 250  
QY 837 GACTTCATTCGCCACCTTCTTGGAACGTGATCCCCAGAAGAGGTTTCACCTGCCAGAGGCC 896  
Db 251 AspPheIleArgHisLeuMetGluLysAspProGluLysArgPheThrCysGluGlnAla 270  
QY 897 CTACAGCATCTTTGGATCTCTGGGATGCAGCCCTTCGATAGGGACATCCTGGGTTCTGTC 956  
Db 271 LeuGlnHisProTrpIleAlaGlyAspThrAlaLeuAspLysAsnIleHisGlnSerVal 290  
QY 957 AGTGAGCAGATCCAGAAGAATTTTGGCAGGACCCCACTGGAAGCGTGCATTCAATGCCACA 1016  
Db 291 SerGluGlnIleLysLysAsnPheAlaLysSerLysTrpLysGlnAlaPheAsnAlaThr 310  
QY 1017 TCATTCTACGTACATCCGTAAG-----CTGGGACAAAGCCCAGAGGGTGAG 1064  
Db 311 AlaValValArgHisMetArgLysLeuGlnLeuGlyThrSerGlnGluGlyGln 328

RESULT 13

Q8AYR3 PRELIMINARY; PRT; 395 AA.

AC Q8AYR3;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Calcium/calmodulin-dependent protein kinase (Cam-KI protein).  
GN Name=Cam-KI;

OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.

RA Saneyoshi T., Kume S., Mikoshiba K.;  
RT "Calcium/calmodulin-dependent protein kinase I in Xenopus laevis.";  
RL Comp. Biochem. Physiol. B, Comp. Biochem. 134:499-507(2003).  
RN [2]  
RP SEQUENCE FROM N.A.

RC TISSUE=Oocytes;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,  
RA Blakesley R.W., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Rodriguez A.C., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [3]  
RP SEQUENCE FROM N.A.





DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR011009; Kinase like.  
DR InterPro; IPR00719; Prot\_kinase.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
DR Pfam; PF00069; Pkinase; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00220; S\_TKc; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 357 AA; 40189 MW; 1FA184EEFA976FB4 CRC64;

Alignment Scores:  
Pred. No.: 1.9e-73 Length: 357  
Score: 1173.50 Matches: 216  
Percent Similarity: 85.09% Conservative: 58  
Best Local Similarity: 67.08% Mismatches: 45  
Query Match: 40.86% Indels: 3  
DB: 2 Gaps: 2

US-10-032-254A-1 (1-1554) x Q9HD31 (1-357)

QY 117 AAGAAACAGACGGAGCATCAGCAGTGTCTATGAGATCGGGAGAAAGCTGGGCTCGGCT 176  
Db 13 LysLysGlnAlaGluAspIleLysLysIlePheGluPheLysGluThrLeuGlyThrGly 32

QY 177 GCCTTCTCTGAGGTGATGCTGGCCAGGAAAGGGCTCTGCTCATCTTGTGGCCCTCAAG 236  
Db 33 AlaPheSerGluValValLeuAlaGluGluLysAlaThrGlyLysLeuPheAlaValLys 52

QY 237 TGCATTCCCAAGAACACTTCGGGGCAAGGAGGCCCTGGTGGAGAATGAGATCGCGGTA 296  
Db 53 CysIleProLysLysAlaLeuLysGlyLysGluSerSerIleGluAsnGluIleAlaVal 72

QY 297 CTTCGCAGAATCAGCCATCCCAACATTGTGGCTCTGGAGAGCTCCATGAGAGTCTTCT 356  
Db 73 LeuArgLysIleLysHisGluAsnIleValAlaLeuGluAspIleTyrGluSerProAsn 92

QY 357 CATCTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAACCTGTTGACCGCATCATGGAG 416  
Db 93 HisLeuTyrLeuValMetGlnLeuValSerGlyGlyGluLeuPheAspArgIleValGlu 112

QY 417 CGSGGCTCTACACAGAGAAGGACGCCACCCACCTTGTAGGCGAGTCTCTGGCGTCTC 476  
Db 113 LysGlyPheTyrThrGluLysAspAlaSerThrLeuIleArgGlnValLeuAspAlaVal 132

QY 477 TCCTACCTTCATAGCCTGGGCATCGTCGACCGGACCTCAAGCCTGAAACCTCCTCTAT 536  
Db 133 TyrTyrLeuHisArgMetGlyIleValHisArgAspLeuLysProGluAsnLeuTyr 152

QY 537 GCCACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTGGCCTGTCCAAAATACAA 596  
Db 153 TyrSerGlnAspGluGluSerLysIleMetIleSerAspPheGlyLeuSerLysMetGlu 172

QY 597 GCT---GGCAACATGCTAGGCACAGCCTGTGGACCCCGAGGATATGTGGCCCGCAGAGCTC 653  
Db 173 GlyLysGlyAspValMetSerThrAlaCysGlyThrProGlyTyrValAlaProGluVal 192

QY 654 CTGAGCAGAAACCCCTACGGGAAGCCCGTAGATGTGTGGGCCCTGGGTGTCATCTCCTAC 713  
Db 193 LeuAlaGlnLysProTyrSerLysAlaValAspCysTrpSerIleGlyValIleAlaTyr 212

QY 714 ATCTGTGTGTGGGTACCCCTTCTCTATGATGAGAGCGATCCTGAACTCTTCAGCCAG 773  
Db 213 IleLeuLeuCysGlyTyrProProPheTyrAspGluAsnAspSerLysLeuPheGluGln 232

QY 774 ATTCTGAGGGCCAGCTATGAGTTTGACTCCCTTTTGGGATGACATCTCAGAAATCAGCC 833  
Db 233 IleLeuLysAlaGluTyrGluPheAspSerProTyrTrpAspAspIleSerAspSerAla 252

QY 834 AAAGACTTCATTGCGCCACCTTCTGGAACGTGATCCCCAGAAAGAGTTTACCTGCCAGCAG 893  
Db 253 LysAspPheIleArgAsnLeuMetGluLysAspProAsnLysArgTyrThrCysGluGln 272

QY 894 GCCTTACAGCATCTTTGGATCTCTGGGGATGCAGCCCTTCGATAGGGACATCTCTGGTTCT 953  
Db 273 AlaAlaArgHisProTrpIleAlaGlyAspThrAlaLeuAsnLysAsnIleHisGluSer 292

QY 954 GTCAGTGAGCAGATCCAGAGAATTTTGCCAGGACCCACTGGAAGCGTGCATTCAATGCC 1013  
Db 293 ValSerAlaGlnIleArgLysAsnPheAlaLysSerLysTrpArgGlnAlaPheAsnAla 312

QY 1014 ACATCATTCCTACGTACATCCGTAAG-----CTGGGACAAAGCCCCAGAGGTTGAGGAG 1067  
Db 313 ThrAlaValValArgHisMetArgLysLeuHisLeuGlySerSerLeuAspSerSerAsn 332

QY 1068 GCCTCC 1073  
Db 333 AlaSer 334

RESULT 15  
Q8IU85  
ID Q8IU85 PRELIMINARY; PRT; 385 AA.  
AC Q8IU85;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, last annotation update)  
DE Calcium/calmodulin-dependent protein kinase ID, beta isoform (CaM-kinase I delta).  
GN Name=CAMKID; Synonyms=CaM-KI delta;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Pancreas;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Pancreas;  
RA Strausberg R.;  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22816754; PubMed=12935886; DOI=10.1016/S0014-5793(03)00817-2;  
RA Ishikawa Y., Tokumitsu H., Inuzuka H., Murata-Hori M., Hosoya H., Kobayashi R.;  
RT "Identification and characterization of novel components of a Ca2+/calmodulin-dependent protein kinase cascade in HeLa cells."  
RL FEBS Lett. 550:57-63(2003).  
RN [4]

RP SEQUENCE FROM N.A.  
RX MEDLINE=20504069; PubMed=11050006;  
RA Verploegen S., Lammers J.L., Koenderman L., Coffey P.J.;  
RT "Identification and characterization of CKIIk, a novel granulocyte  
RT Ca+/calmodulin-dependent protein kinase.";  
RL Blood 96:3215-3223(2000).  
CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.  
DR EMBL; BC035745; AAH35745.1; -.  
DR EMBL; AB081726; BAC19846.1; -.  
DR HSSP; Q63450; 1A06.  
DR Genew; HGNC:19341; CAMK1D.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.  
DR GO; GO:0016740; F:transferase activity; IEA.  
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.  
DR InterPro; IPR011009; Kinase like.  
DR InterPro; IPR000719; Prot\_kinase.  
DR InterPro; IPR002290; Ser\_thr\_pkinase.  
DR InterPro; IPR008271; Ser\_thr\_pkin\_AS.  
DR Pfam; PF00069; Pkinase; 1.  
DR ProDom; PD000001; Prot\_kinase; 1.  
DR SMART; SM00220; S\_TKC; 1.  
DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE; PS00111; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 385 AA; 42913 MW; 717467D019E30FC9 CRC64;

Alignment Scores:

Pred. No.:	1.94e-73	Length:	385
Score:	1173.50	Matches:	216
Percent Similarity:	85.09%	Conservative:	58
Best Local Similarity:	67.08%	Mismatches:	45
Query Match:	40.86%	Indels:	3
DB:	2	Gaps:	2

US-10-032-254A-1 (1-1554) x Q8IU85 (1-385)

QY	117	AAGAAACAGACGGAGGACATCAGCAGTGTCTATGATCCGGGAGAGCTGGGCTCGGGT	176
Db	13	LysLysGlnAlaGluAspLeLysLysIlePheGluPheLysGluThrLeuGlyThrGly	32
QY	177	GCCTTCTCTGAGGTGATGTGGCCCCAGGAAAGGGCTCTGCTCATCTTGTGGCCCTCAAG	236
Db	33	AlaPheSerGluValValLeuAlaGluGluLysAlaThrGlyLysLeuPheAlaValLys	52
QY	237	TGCATTCCCAAGAACACTTCGGGGCAAGGAGGCCCTGGTGAGAAATGAGATCGCGGTA	296
Db	53	CysIleProLysLysAlaLeuLysGlyLysGluSerSerIleGluAsnGluIleAlaVal	72
QY	297	CTTCGCAGAATCAGCCATCCCAACATTGTGGCTCTGGAGGACGTCCATGAGAGTCCTTCT	356
Db	73	LeuArgLysIleLysHisGluAsnIleValAlaLeuGluAspIleTyrGluSerProAsn	92
QY	357	CATCTCTACTTGGCCATGGAGCTGGTAACAGGTGGTGAAGTGTGACCGCATCATGGAG	416
Db	93	HisLeuTyrLeuValMetGlnLeuValSerGlyGlyGluLeuPheAspArgIleValGlu	112
QY	417	CGGGGCTCCTACACAGAGAGGACGCCACCTTTAGGGCAGGTCCTTGGCGGTGTC	476
Db	113	LysGlyPheTyrThrGluLysAspAlaSerThrLeuIleArgGlnValLeuAspAlaVal	132
QY	477	TCCTACCTTCATAGCCTGGGATCGTGCACCGGACCTCAAGCCTGAAACCTCCTCTAT	536
Db	133	TyrTyrLeuHisArgMetGlyIleValHisArgAspLeuLysProGluAsnLeuTyr	152
QY	537	GCCACACCTTTTGAGGACTCCAAGATCATGGTCTCTGACTTTGGCCTGTCCAAAATACAA	596
Db	153	TyrSerGlnAspGluGluSerLysIleMetIleSerAspPheGlyLeuSerLysMetGlu	172
QY	597	GCT--GGCAACATGCTAGGCACAGCCTGTGGGACCCCAAGGATATGTGGCCCCAGAGCTC	653
Db	173	GlyLysGlyAspValMetSerThrAlaCysGlyThrProGlyTyrValAlaProGluVal	192

QY	654	CTGGAGCAGAAACCCCTACGGGAAGGCGGTAGATGTGTGGGCCCTGGGTGTCATCTCCTAC	713
Db	193	LeuAlaGlnLysProTyrSerLysAlaValAspCysTrpSerIleGlyValIleAlaTyr	212
QY	714	ATCCTGTCTGTGGGTACCCCCCTTCTATGATGAGAGCGATCCTGAACCTTCAGCCAG	773
Db	213	IleLeuLeuCysGlyTyrProProPheTyrAspGluAsnAspSerLysLeuPheGluGln	232
QY	774	ATTCTGAGGCGCAGCTATGAGTTTGACTCCCCCTTTTGGGATGACATCTCAGAATCAGCC	833
Db	233	IleLeuLysAlaGluTyrGluPheAspSerProTyrTrpAspAspIleSerAspSerAla	252
QY	834	AAAGACTTCATTGCGCCACCTTCTGGAACGTGATCCCCAGAGAGTTTCACTGCCAGCAG	893
Db	253	LysAspPheIleArgAsnLeuMetGluLysAspProAsnLysArgTyrThrCysGluGln	272
QY	894	GCCCTACAGCATCTTTGGATCTCTGGGGATGCAGCCCTTCGATAGGGACATCTGGGTTCT	953
Db	273	AlaAlaArgHisProTrpIleAlaGlyAspThrAlaLeuAsnLysAsnIleHisGluSer	292
QY	954	GTCAGTGAGCAGATCCAGAAAGAAATTTTGCAGGACCCACTGGAAGCGTGCAATCAATGCC	1013
Db	293	ValSerAlaGlnIleArgLysAsnPheAlaLysSerLysTrpArgGlnAlaPheAsnAla	312
QY	1014	ACATCATTCCTACGTCCATCCGTAAG-----CTGGGACAAAAGCCAGAGGGGTGAGGAG	1067
Db	313	ThrAlaValValArgHisMetArgLysLeuHisLeuGlySerSerLeuAspSerSerAsn	332
QY	1068	GCCTCC	1073
Db	333	AlaSer	334

Search completed: June 6, 2005, 11:58:34  
Job time : 247 secs